

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 09:39:40 ; Search time 83 seconds
(without alignments)
15.299 Million cell updates/sec

Title: US-10-056-052A-29

Perfect score: 44

Sequence: 1 HQYLSSYT 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

1107863 seqs, 158726573 residues
1107863
All number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_19Jun03.*

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22: /SIDSL/gcgdata/geneseq/geneseq-embl/AA2001.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-embl/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-embl/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 44 | 100.0 | 8 | AAE29276 | Anti-ClfA monoclon |
| 2 | 44 | 100.0 | 112 | AAE29266 | S. aureus ClfA spe |
| 3 | 44 | 100.0 | 112 | AAE29268 | S. aureus ClfA spe |
| 4 | 44 | 100.0 | 112 | AAE29270 | S. aureus ClfA spe |
| 5 | 39 | 88.6 | 112 | AAR54932 | Pc receptor humani |
| 6 | 39 | 88.6 | 112 | AAR54933 | Mab 022 VK chain. |
| 7 | 39 | 88.6 | 112 | AAE29264 | S. aureus ClfA spe |
| 8 | 39 | 88.6 | 113 | AAR92215 | LL2 Mab VK region. |
| 9 | 39 | 88.6 | 113 | AAR92217 | Humanised LL2 Mab |

| | | | | | | |
|----|----|------|------|----|----------|--------------------|
| 10 | 39 | 88.6 | 113 | 18 | AAW27695 | Variable kappa cha |
| 11 | 39 | 88.6 | 115 | 18 | AAW27697 | Variable kappa cha |
| 12 | 39 | 88.6 | 263 | 20 | AAW90226 | Anti-B7.2 monospec |
| 13 | 39 | 88.6 | 268 | 20 | AAW90228 | Anti-B7.1/anti-B7. |
| 14 | 39 | 88.6 | 268 | 20 | AAW90222 | Anti-B7.2 monospec |
| 15 | 39 | 88.6 | 273 | 20 | AAW90224 | Anti-B7.1/anti-B7. |
| 16 | 39 | 88.6 | 301 | 18 | AAW11507 | Single chain, huma |
| 17 | 39 | 88.6 | 301 | 20 | AAW73217 | Multispecific sing |
| 18 | 39 | 88.6 | 301 | 22 | AAW85454 | Single chain human |
| 19 | 39 | 88.6 | 301 | 22 | AAW61959 | Single chain human |
| 20 | 39 | 88.6 | 352 | 20 | AAW06272 | Anti-Fc gamma rece |
| 21 | 39 | 88.6 | 553 | 18 | AAW11508 | Single chain anti- |
| 22 | 39 | 88.6 | 553 | 20 | AAW73223 | H22-anti-CEA antib |
| 23 | 39 | 88.6 | 553 | 22 | AAW85455 | Bispecific single |
| 24 | 39 | 88.6 | 553 | 22 | AAW61960 | Bispecific single |
| 25 | 39 | 88.6 | 556 | 20 | AAW90218 | Bispecific tetra |
| 26 | 39 | 88.6 | 580 | 20 | AAW90217 | Bispecific tetra |
| 27 | 36 | 81.8 | 112 | 23 | ABG70739 | Variable chain of |
| 28 | 36 | 81.8 | 238 | 23 | ABG70744 | Mouse/human chim |
| 29 | 35 | 79.5 | 272 | 23 | ABG31024 | Synthetic mouse fu |
| 30 | 34 | 77.3 | 86 | 22 | AAW99674 | Human excretory re |
| 31 | 34 | 77.3 | 86 | 22 | AAW42489 | Human kidney relat |
| 32 | 34 | 77.3 | 468 | 21 | AAW75187 | Neisseria meningit |
| 33 | 34 | 77.3 | 543 | 22 | ABW71263 | Drosophila melanog |
| 34 | 33 | 75.0 | 330 | 22 | ABW57984 | Drosophila melanog |
| 35 | 33 | 75.0 | 554 | 18 | AAW01824 | Manduca sexta larv |
| 36 | 33 | 75.0 | 554 | 21 | AAW07183 | Manduca sexta gut |
| 37 | 33 | 75.0 | 554 | 24 | ABP72619 | Manduca sexta chit |
| 38 | 33 | 75.0 | 921 | 21 | AAW32297 | Corn polycomb prot |
| 39 | 33 | 75.0 | 931 | 23 | AAO14529 | Protein of Mezi (M |
| 40 | 33 | 75.0 | 1369 | 22 | ABW60839 | Drosophila melanog |
| 41 | 33 | 75.0 | 2308 | 15 | AAW52580 | RPTP-beta amino ac |
| 42 | 32 | 72.7 | 52 | 23 | ABP03502 | Human ORFX protein |
| 43 | 32 | 72.7 | 210 | 21 | AAW34736 | Human secreted pro |
| 44 | 32 | 72.7 | 226 | 24 | ABJ19085 | Pathogen specific |
| 45 | 32 | 72.7 | 235 | 22 | AAU33959 | Staphylococcus aur |

ALIGNMENTS

RESULT 1

AAE29276

ID AAE29276 standard; peptide: 8 AA.

XX AAE29276;

AC AAE29276;

XX AAE29276;

DT 27-JAN-2003 (first entry)

XX Anti-ClfA monoclonal antibody variable light chain CDR3.

DE Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;

KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;

KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy;

KW complementarity determining region; CDR.

OS Unidentified.

XX WO200272600-A2.

XX 19-SEP-2002.

XX 28-JAN-2002; 2002WO-US02296.

XX 26-JAN-2001; 2001US-264072P.

XX 12-MAR-2001; 2001US-274611P.

XX 30-JUN-2001; 2001US-298413P.

XX 30-JUL-2001; 2001US-308116P.

XX (INHI-) INHIBITEX INC.

XX Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;

XX

WPI: 2002-759834/82.

New anti-clumping factor A (ClfA) monoclonal antibody, useful for treating or preventing *Staphylococcus aureus* infection e.g. wound infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in a human or animal

Claim 31; Page 55; 80pp: English.

The invention relates to monoclonal antibody which binds the clumping factor A (ClfA) protein from *Staphylococcus aureus*. The anti-ClfA monoclonal antibody is useful for treating or preventing *S. aureus* infection in a human or animal, and for inhibiting the binding of staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment *S. aureus* Clf40 protein, *S. aureus* Clf33 protein, or the *S. aureus* N3 protein is useful for inducing an immunological response in a human or animal. These staphylococcal infections include wound infections, sepsis, impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The present sequence is an anti-ClfA monoclonal antibody variable light chain complementarity determining region (CDR).

Query Match 100.0%; Score 44; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | |
|----------|---|
| RESULT_2 | |
| AAE29266 | |
| ID | AAE29266 standard; Protein; 112 AA. |
| XX | |
| PAC | |
| XX | AAE29266; |
| DT | 27-JAN-2003 (first entry) |
| XX | |
| DE | S. aureus ClfA specific monoclonal antibody 12-9VIA-1 protein. |
| XX | |
| KW | Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein; |
| KW | immunological; staphylococcal infection; impetigo; pneumonia; furuncle; |
| KW | septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy. |
| XX | |
| PS | Staphylococcus aureus. |

XX PT PT PT PT XX PS XX CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC XX SQ

Q B M Qy Db

RES00
AAEJID
XXAC
XXOT
XXDE
XXKW
XW
XW
XS
XH
TT
TT
TT
TT
TX
NX
DX
FX
RR
RR
RR
RX
AX
IX
RR
RX

PT New anti-clumping factor A (ClfA) monoclonal antibody, useful for
 PT treating or preventing Staphylococcus aureus infection e.g. wound
 PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis
 PT in a human or animal
 XX
 PS Claim 11; Page 37; 80pp; English.
 XX
 CC The invention relates to monoclonal antibody which binds the clumping
 CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
 CC monoclonal antibody is useful for treating or preventing S. aureus
 CC infection in a human or animal, and for inhibiting the binding of
 CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
 CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
 CC protein is useful for inducing an immunological response in a human or
 CC animal. These staphylococcal infections include wound infections, sepsis,
 CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
 CC present sequence is Staphylococcus aureus ClfA specific monoclonal
 CC antibody 35-220VLD-4 (variable light sequence) protein.

Sequence 112 AA;

Query Match 100.0%; Score 44; DB 23; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.28; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0;

Qy 1 HQYLSSYT 8
 |||||
 Db 95 HQYLSSYT 102

RESULT 4
 AAE29270
 ID AAE29270 standard; Protein: 112 AA.

XX AC AAE29270;

DT 27-JAN-2003 (first entry)

DE S. aureus ClfA specific monoclonal antibody 12-9VL-Hu protein.

XX Clumping factor A: ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
 KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
 KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.

OS Staphylococcus aureus.

XX Key Location/Qualifiers

Region 24..40

Region /note= "CDR1"

Region /note= "CDR2"

Region /note= "CDR3"

XX WO200272600-A2.

XX 19-SEP-2002.

XX 28-JAN-2002; 2002WO-US02296.

XX 26-JAN-2001; 2001US-264072P.

XX 12-MAR-2001; 2001US-274611P.

XX 18-JUN-2001; 2001US-298413P.

XX 30-JUL-2001; 2001US-308116P.

XX (INH1-) INHIBITEX INC.

XX Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;

XX WPI; 2002-759834/82.

XX N-PSDB; AAD46869.

PT New anti-clumping factor A (ClfA) monoclonal antibody, useful for

PT treating or preventing Staphylococcus aureus infection e.g. wound
 PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis
 PT in a human or animal
 XX
 PS Claim 11; Page 42; 80pp; English.
 XX
 CC The invention relates to monoclonal antibody which binds the clumping
 CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
 CC monoclonal antibody is useful for treating or preventing S. aureus
 CC infection in a human or animal, and for inhibiting the binding of
 CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
 CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
 CC protein is useful for inducing an immunological response in a human or
 CC animal. These staphylococcal infections include wound infections, sepsis,
 CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
 CC present sequence is Staphylococcus aureus ClfA specific monoclonal
 CC antibody 12-9VL-Hu (humanised variable light sequence) protein.

XX Sequence 112 AA;

Query Match 100.0%; Score 44; DB 23; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.28; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0;

Qy 1 HQYLSSYT 8
 |||||
 Db 95 HQYLSSYT 102

RESULT 5

AAR54932
 ID AAR54932 standard; peptide: 112 AA.

XX AC AAR54932;

DT 25-MAR-2003 (updated)

DT 19-OCT-1994 (first entry)

DE Fc receptor humanized VK chain 022 HuVK.

XX Fc receptor; FcR; humanized antibody; hAb; IgG; cancer; allergy;
 KW autoimmune disease; heteroantibody; bifunctional antibody;
 KW immunotoxin; CDR; complementarity determining region; VH;
 KW heavy chain variable region; VK; kappa chain variable region;
 KW mononuclear phagocyte; PCR; polymerase chain reaction; primer;
 KW site-directed mutagenesis; HuVK; monoclonal antibody; MAb.

XX Homo sapiens; Mus sp.

XX WO9410332-A1.

XX 11-MAY-1994.

XX 04-NOV-1993; 93WO-US10384.

XX 04-NOV-1992; 92GB-0023377.

XX (MEDA-) MEDAREX INC.

XX Carr FJ, Harris WJ, Tempest PR;

XX WPI; 1994-167486/20.

XX New humanised antibodies to Fc receptors - used for diagnosis or
 PT for treatment of e.g. cancer, allergies and infectious and
 PT auto-immune diseases

XX Disclosure; Page 16; 36pp; English.

XX Humanized antibodies (hAbs) for IgG Fc receptors on human phagocytes
 CC comprise the CDR of mouse monoclonal antibody 22 (from hybridoma
 CC 022WCL-1). VH chains from human Igs NEWM or KOL, and VK chains from
 CC Ig REI. Sequences are provided for mouse 022 VH (AAR54931),

CC humanized NEWM-based VH (022 NMVH, AAR54929), humanized KOL-
 CC based VH (022 KLVH, AAR54930), mouse 022 VK (AAR54933) and humanized
 CC REI- based VH (022 HuVK, AAR54932). During hab production, VH and VK
 CC cDNAs were PCR amplified using primers given in AAQ65378-87.
 CC Mutagenesis of clone M13VHPCR2 KOL VH (L71R) was performed using
 CC oligos AAQ65388-89. The HABS can be used in heteroantibody,
 CC bifunctional antibody and immunotoxin production.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX

SO Sequence 112 AA;

Query Match 88.6%; Score 39; DB 15; Length 112;
 Best Local Similarity 87.5%; Pred. No. 2.8;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSSYT 8
 Db 95 HOYLSSWT 102
 |||||:|

RESULT 6

AA54933
 AAR54933 standard; peptide; 112 AA.

AC AAR54933;

DT 25-MAR-2003 (updated)

DT 19-OCT-1994 (first entry)

DE Mab 022 VK chain.

KW Fc receptor; FcR; humanized antibody; hab; IgG; cancer; allergy;
 KW autoimmune disease; heteroantibody; bifunctional antibody;
 KW immunotoxin; CDR; complementarity determining region; VH;
 KW heavy chain variable region; VK; kappa chain variable region;
 KW mononuclear phagocyte; PCR; polymerase chain reaction; primer;
 KW site-directed mutagenesis; monoclonal antibody; Mab.

OS Mus sp.

XX WO9410332-A1.

XX 11-MAY-1994.

XX 04-NOV-1993; 93WO-US10384.

XX 04-NOV-1992; 92GB-0023377.

XX (MEDA-) MEDAREX INC.

XX Carr FJ, Harris WJ, Tempest PR;

XX WPI; 1994-167486/20..

XX New humanised antibodies to Fc receptors - used for diagnosis or
 XX for treatment of e.g. cancer, allergies and infectious and
 XX auto-immune diseases

XX Disclosure; Page 23; 36pp; English.

XX Humanized antibodies (hAbs) for IgG Fc receptors on human phagocytes
 XX comprise the CDR of mouse monoclonal antibody 22 (from hybridoma
 XX 022WGL-1), VH chains from human IgG NEWM or KOL, and VK chains from
 XX Ig REI. Sequences are provided for mouse 022 VH (AAR54931),
 XX humanized NEWM-based VH (022 NMVH, AAR54929), humanized KOL-
 XX based VH (022 KLVH, AAR54930), mouse 022 VK (AAR54933) and humanized
 XX REI- based VH (022 HuVK, AAR54932). During hab production, VH and VK
 XX cDNAs were PCR amplified using primers given in AAQ65378-87.
 XX Mutagenesis of clone M13VHPCR2 KOL VH (L71R) was performed using
 XX oligos AAQ65388-89. The HABS can be used in heteroantibody,
 XX bifunctional antibody and immunotoxin production.
 XX (Updated on 25-MAR-2003 to correct PN field.)

SO Sequence 112 AA;

Query Match 88.6%; Score 39; DB 15; Length 112;
 Best Local Similarity 87.5%; Pred. No. 2.8;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSSYT 8
 Db 95 HOYLSSWT 102
 |||||:|

RESULT 7

AAE29264

ID AAE29264 standard; Protein; 112 AA.

XX AAE29264;

XX 27-JAN-2003 (first entry)

DE S. aureus ClfA specific monoclonal antibody 13-2VLA-1 protein.

XX Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
 KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
 KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.

OS Staphylococcus aureus.

XX Key Location/Qualifiers

FT Region 24..40

FT /note= "CDR1"

FT Region 56..62

FT /note= "CDR2"

FT Region 95..102

FT /note= "CDR3"

XX WO200272600-A2.

XX 19-SEP-2002.

XX 28-JAN-2002; 2002WO-US02296.

XX 26-JAN-2001; 2001US-264072P.

XX 12-MAR-2001; 2001US-274611P.

XX 18-JUN-2001; 2001US-298413P.

XX 30-JUL-2001; 2001US-308116P.

XX (INH1-) INHIBITEX INC.

XX Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;

XX WPI; 2002-759834/82.

XX N-PSDB; AAD46863.

XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
 XX treating or preventing Staphylococcus aureus infection e.g. wound
 XX infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis
 XX in a human or animal

XX Claim 11; Page 34; 80pp; English.

XX The invention relates to monoclonal antibody which binds the clumping
 XX factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
 XX monoclonal antibody is useful for treating or preventing S. aureus
 XX infection in a human or animal, and for inhibiting the binding of
 XX staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
 XX S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
 XX protein is useful for inducing an immunological response in a human or
 XX animal. These staphylococcal infections include wound infections, sepsis,
 XX impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
 XX present sequence is Staphylococcus aureus ClfA specific monoclonal
 XX antibody 13-2VLA-1 (variable light sequence) protein.

XX Sequence 112 AA;

Query Match 88.6%; Score 39; DB 23; Length 112;
 Best Local Similarity 87.5%; Pred. No. 2.8;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSSYT 8
 DB 95 HOYLSSWT 102

RESULT 8
 AAR92215
 ID AAR92215 standard; Protein; 113 AA.
 XX
 AC AAR92215;
 XX
 DT 28-MAY-1996 (first entry)
 XX
 DE LL2 MAB VK region.
 XX
 KW Humanised antibody; monoclonal antibody; MAB; LL2; B-cell lymphoma;
 KW leukaemia; therapy; diagnosis; complementarity determining region;
 KW CDR; antibody engineering.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 24..40
 FT /label= CDR1
 FT Region 56..62
 FT /label= CDR2
 FT Region 95..103
 FT /label= CDR3
 FT WO9604925-A1.
 PN
 XX
 XX 22-FEB-1996.
 PD
 XX
 PF 11-AUG-1995; 95WO-US09641.
 XX
 XX 12-AUG-1994; 94US-0289576.
 PR
 XX
 PA (IMMU-) IMMUNOMEDICS INC.
 XX
 PI Hansen H, Leung S;
 XX
 DR WPI; 1996-139454/14.
 DR N-PSDB; AAT15802.
 XX
 PT Chimeric and humanised LL2 antibodies - used to produce conjugates
 PT for the therapy and diagnosis of B-cell lymphoma(s) and
 PT leukaemia(s).
 XX
 PS Claim 5; Page 35-36; 70pp; English.
 XX
 CC The complementarity determining regions (CDRs) of mouse monoclonal
 CC antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were
 CC recombinantly linked to the framework sequences of human VK and VH
 CC regions, respectively, to give humanised LL2 VK (AAR92217) and VH
 CC (AAR92218). These were subsequently linked, respectively, to human
 CC kappa and IgG1 constant regions. A humanised Mab was obtd. that
 CC retained the B-lymphoma and leukaemia cell targeting and
 CC internalisation characteristics of the parental LL2 MAB, and which
 CC exhibited a lowered HAMA reaction. It can be linked to e.g. a
 CC cytostatic agent for therapeutic appln.
 XX
 SQ Sequence 113 AA;

Query Match 88.6%; Score 39; DB 17; Length 113;
 Best Local Similarity 87.5%; Pred. No. 2.8;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSSYT 8
 DB 95 HOYLSSWT 102

RESULT 9
 AAR92217
 ID AAR92217 standard; Protein; 113 AA.
 XX
 AC AAR92217;
 XX
 DT 28-MAY-1996 (first entry)
 XX
 DE Humanised LL2 MAB VK region.
 XX
 KW Humanised antibody; monoclonal antibody; MAB; LL2; B-cell lymphoma;
 KW leukaemia; therapy; diagnosis; complementarity determining region;
 KW CDR; antibody engineering.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 24..40
 FT /label= CDR1
 FT Region 56..62
 FT /label= CDR2
 FT Region 95..103
 FT /label= CDR3
 FT WO9604925-A1.
 PN
 XX
 XX 22-FEB-1996.
 PD
 XX
 PF 11-AUG-1995; 95WO-US09641.
 XX
 XX 12-AUG-1994; 94US-0289576.
 PR
 XX
 PA (IMMU-) IMMUNOMEDICS INC.
 XX
 PI Hansen H, Leung S;
 XX
 DR WPI; 1996-139454/14.
 DR N-PSDB; AAT15803.
 XX
 PT Chimeric and humanised LL2 antibodies - used to produce conjugates
 PT for the therapy and diagnosis of B-cell lymphoma(s) and
 PT leukaemia(s).
 XX
 PS Claim 5; Page 38; 70pp; English.
 XX
 CC The complementarity determining regions (CDRs) of mouse monoclonal
 CC antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were
 CC recombinantly linked to the framework sequences of human VK and VH
 CC regions, respectively, to give humanised LL2 VK (AAR92217) and VH
 CC (AAR92218). These were subsequently linked, respectively, to human
 CC kappa and IgG1 constant regions. A humanised Mab was obtd. that
 CC retained the B-lymphoma and leukaemia cell targeting and
 CC internalisation characteristics of the parental LL2 MAB, and which
 CC exhibited a lowered HAMA reaction. It can be linked to e.g. a
 CC cytostatic agent for therapeutic appln.
 XX
 SQ Sequence 113 AA;

Query Match 88.6%; Score 39; DB 17; Length 113;
 Best Local Similarity 87.5%; Pred. No. 2.8;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSSYT 8
 DB 95 HOYLSSWT 102

RESULT 10

AAW27695
 ID AAW27695 standard; Protein; 113 AA.
 XX
 AC AAW27695;
 XX
 DT 14-APR-1998 (first entry)
 XX
 DE Variable kappa chain of MAB LL2.
 XX
 DE Variable kappa chain; B cell; monoclonal antibody; MAB; LL2;
 KW B cell lymphoma; lymphocytic leukaemia cell; murine;
 KW diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
 KW chronic lymphocytic leukaemia.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 FH Key
 FT Region 18..20
 FT /note= "potential N-linked glycosylation site"
 FT Region 24..40
 FT /note= "complementarity determining region 1"
 FT Region 56..62
 FT /note= "complementarity determining region 2"
 FT Region 95..102
 FT /note= "complementarity determining region 3"
 FT
 XX W09734632-A1.
 PN 25-SEP-1997.
 XX
 PD 19-MAR-1997; 97WO-US04196.
 XX
 PR 20-MAR-1996; 96US-0013709.
 XX
 PA (IMMU-) IMMUNOMEDICS INC.
 XX
 PI Hansen H, Leung S, Qu Z;
 XX
 DR WPI; 1997-479995/44.
 DR N-PSDB; AAT88128.
 XX
 PT Monoclonal antibody engineered to contain glycosylation site - in
 PT non-Fc constant heavy or light chain region, useful to diagnose or
 PT treat B cell malignancies, e.g. non-Hodgkins lymphoma
 XX
 PS Example 3; Fig 4A; 88pp; English.
 CC The present sequence is the variable kappa chain of the
 CC B cell specific monoclonal antibody (Mab) LL2, which contains an
 CC engineered tri-peptide N-glycan acceptor sequence. LL2 is a highly
 CC specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell
 CC murine Mab. The Mab can be used to diagnose or treat B
 CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic
 CC lymphocytic leukaemia. The glycosylation site allows a label or
 CC therapeutic agent of increased size to be conjugated to the
 CC carbohydrate moiety, without affecting the Mab's binding affinity
 CC or specificity.
 XX
 SQ Sequence 113 AA;
 Query Match 88.6%; Score 39; DB 18; Length 113;
 Best Local Similarity 87.5%; Pred. No. 2.8;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HOYLSSYT 8
 DB 95 HOYLSSWT 102

RESULT 11

AAW27697
 ID AAW27697 standard; Protein; 115 AA.
 XX
 AC AAW27697;
 XX
 DT 14-APR-1998 (first entry)
 XX
 DE Variable kappa chain of MAB hLL2.
 XX
 DE Variable kappa chain; B cell; monoclonal antibody; MAB; hLL2;
 KW B cell lymphoma; lymphocytic leukaemia cell; murine; humanised;
 KW diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
 KW chronic lymphocytic leukaemia.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 FH Key
 FT Region 24..40
 FT /note= "complementarity determining region 1"
 FT Region 56..62
 FT /note= "complementarity determining region 2"
 FT Region 95..102
 FT /note= "complementarity determining region 3"
 FT
 XX W09734632-A1.
 PN 25-SEP-1997.
 XX
 PD 19-MAR-1997; 97WO-US04196.
 XX
 PR 20-MAR-1996; 96US-0013709.
 XX
 PA (IMMU-) IMMUNOMEDICS INC.
 XX
 PI Hansen H, Leung S, Qu Z;
 XX
 DR WPI; 1997-479995/44.
 DR N-PSDB; AAT88130.
 XX
 PT Monoclonal antibody engineered to contain glycosylation site - in
 PT non-Fc constant heavy or light chain region, useful to diagnose or
 PT treat B cell malignancies, e.g. non-Hodgkins lymphoma
 XX
 PS Example 3; Fig 5A; 88pp; English.
 CC The present sequence is the variable kappa chain of the
 CC B cell specific monoclonal antibody (MAB) hLL2. hLL2 is a highly
 CC specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell
 CC humanised murine Mab. The Mab can be used to diagnose or treat B
 CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic
 CC lymphocytic leukaemia.
 XX
 SQ Sequence 115 AA;
 Query Match 88.6%; Score 39; DB 18; Length 115;
 Best Local Similarity 87.5%; Pred. No. 2.9;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HOYLSSYT 8
 DB 95 HOYLSSWT 102

RESULT 12

AAW90226
 ID AAW90226 standard; Protein; 263 AA.
 XX
 AC AAW90226;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Anti-B7.2 monospecific triabody 1G10.

XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
 KW CD86; T cell activation; inhibitor; graft versus host disease;
 KW transplant rejection; allograft rejection; autoimmune disease;
 XX allergy; therapy; human; triabody; antibody; Ig10.
 OS Chimeric - Mus sp.
 OS Chimeric - synthetic.

XX Key Location/Qualifiers
 FT Peptide 1..24
 FT /note= "pelB signal peptide"
 FT Region 25..144
 FT /note= "anti B7.2 MAB VH region"
 FT Peptide 145..257
 FT /note= "anti B7.2 MAB VL region"
 FT Peptide 258..263
 FT /note= "His6 tag"

XX WO9858965-A2.

XX 30-DEC-1998.

XX 22-JUN-1998; 98WO-EP03791.

XX 20-JUN-1997; 97EP-0870092.

XX (INNO-) INNOGENETICS NV.

XX Bosman A, Buyse M, Lorre K, Sablon E;

XX WPI: 1999-105615/09.

XX N-PSDB; AAX01660.

XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
 PT immune diseases including allograft rejection

XX Example 7.3; Fig 34; 182pp; English.

XX This polypeptide comprises a Ig10 monospecific triabody composed
 CC of the VH region of anti-B7.2 monoclonal antibody (MAB) Ig10
 CC joined to the VL region of Ig10. A triabody is a mono- a bi- or
 CC a trispecific molecule recognising simultaneously e.g. two B7.2
 CC and one B7.1 molecules. It has a rigid structure that prevents
 CC simultaneous binding to the 3 targets. Each antigen-binding site
 CC is formed by pairing of one VH and one VL domain from the same or
 CC from two different polypeptides. The invention relates to novel
 CC molecules, including triabodies, which can cross-link and/or
 CC cross-react with the costimulatory molecules B7.1 and B7.2 expressed
 CC on professional antigen-presenting cells, leading to the inhibition
 CC of antigen-specific T cell activation. Methods are provided for
 CC the production of such B7-binding molecules, and for their use in
 CC the treatment or prevention of diseases of the immune system, in
 CC particular graft rejection, graft versus host disease, allergy and
 CC autoimmune diseases (claimed).

XX Sequence 263 AA;

Query Match 88.6%; Score 39; DB 20; Length 263;

Best Local Similarity 87.5%; Pred. No. 7.1;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSVT 8

DB 239 HQYLSSWT 246

RESULT 13

AAW90228

ID AAW90228 standard; Protein; 268 AA.

XX AC AAW90228;

XX

DT 10-MAY-1999 (first entry)

XX Anti-B7.1/anti-B7.2 bispecific triabody II.

XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
 KW CD86; T cell activation; inhibitor; graft versus host disease;
 KW transplant rejection; allograft rejection; autoimmune disease;
 KW allergy; therapy; human; triabody; antibody; B7-24; Ig10.

XX Chimeric - Mus sp.

OS Chimeric - synthetic.

XX Key Location/Qualifiers

FT Peptide 1..39

FT /note= "g3p signal peptide"

FT Region 40..155

FT /note= "anti B7.1 MAB VH region"

FT Peptide 156..268

FT /note= "anti B7.2 MAB VL region"

XX WO9858965-A2.

XX 30-DEC-1998.

XX 22-JUN-1998; 98WO-EP03791.

XX 20-JUN-1997; 97EP-0870092.

XX (INNO-) INNOGENETICS NV.

XX Bosman A, Buyse M, Lorre K, Sablon E;

XX WPI: 1999-105615/09.

XX N-PSDB; AAX01662.

XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
 PT immune diseases including allograft rejection

XX Example 7.3; Fig 38; 182pp; English.

XX This polypeptide comprises a bispecific triabody composed of the VH
 CC region of anti-B7.1 monoclonal antibody (MAB) B7-24 joined to the
 CC VL region of anti-B7.2 MAB Ig10. A triabody is a mono- a bi- or
 CC a trispecific molecule recognising simultaneously e.g. two B7.2
 CC and one B7.1 molecules. It has a rigid structure that prevents
 CC simultaneous binding to the 3 targets. Each antigen-binding site
 CC is formed by pairing of one VH and one VL domain from the same or
 CC from two different polypeptides. The invention relates to novel
 CC molecules, including triabodies, which can cross-link and/or
 CC cross-react with the costimulatory molecules B7.1 and B7.2 expressed
 CC on professional antigen-presenting cells, leading to the inhibition
 CC of antigen-specific T cell activation. Methods are provided for
 CC the production of such B7-binding molecules, and for their use in
 CC the treatment or prevention of diseases of the immune system, in
 CC particular graft rejection, graft versus host disease, allergy and
 CC autoimmune diseases (claimed).

XX Sequence 268 AA;

Query Match 88.6%; Score 39; DB 20; Length 268;

Best Local Similarity 87.5%; Pred. No. 7.2;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSVT 8

DB 250 HQYLSSWT 257

RESULT 14

AAW90222

ID AAW90222 standard; Protein; 268 AA.

XX AC AAW90222;

XX

XX 10-MAY-1999 (first entry)
XX Anti-B7.2 monospecific diabody 1G-10.
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX CD86; T cell activation; inhibitor; graft versus host disease;
XX transplant rejection; allograft rejection; autoimmune disease;
XX allergy; therapy; human; diabody; antibody; 1G-10.
XX Chimeric - Mus sp.
XX Chimeric - synthetic.
XX Key Location/Qualifiers
XX Peptide 1..24
XX Region 25..144
XX Peptide /note= "anti B7.2 Mab VH region"
XX Region 145..149
XX Peptide /note= "G4S flexible linker"
XX Region 150..262
XX Peptide /note= "anti B7.2 Mab VL region"
XX Region 263..268
XX Peptide /note= "His6 tag"
XX WO9858965-A2.
XX 30-DEC-1998.
XX 22-JUN-1998; 98WO-EP03791.
XX 20-JUN-1997; 97EP-0870092.
XX (INNO-) INNOGENETICS NV.
XX Bosman A, Buyse M, Lorre K, Sablon E;
XX WPI: 1999-105615/09.
XX N-PSDB: AAX01656.
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX immune diseases including allograft rejection
XX Example 7.2; Fig 26; 182pp; English.
XX This polypeptide comprises a 1G-10 monospecific diabody composed
XX of the VH region of anti-B7.2 monoclonal antibody (Mab) 1G-10
XX joined via a short, flexible linker to the VL region of 1G-10.
XX Mono- or bispecific bivalent molecules are generated by shortening
XX the flexible linker sequence between the VH and VL of the anti-B7.1
XX scFv B7-24, the anti-B7.2 scFv 1G10 and the scFv molecule with
XX dual specificity for B7.1 and B7.2 (B7.12) to 5-10 residues, and
XX for bispecific molecules by cross-pairing the VH and VL domains
XX from the 2 scFvs with different antigen recognition (B7.1/B7.2 and
XX B7.12/B7.12). The invention relates to novel molecules, including
XX diabodies, which can cross-link and/or cross-react with the
XX costimulatory molecules B7.1 and B7.2 expressed on professional
XX antigen-presenting cells, leading to the inhibition of antigen-
XX specific T cell activation. Methods are provided for the
XX production of such B7-binding molecules, and for their use in the
XX treatment or prevention of diseases of the immune system, in
XX particular graft rejection, graft versus host disease, allergy and
XX autoimmune diseases (claimed).
XX Sequence 268 AA;
Query Match 88.6%; Score 39; DB 20; Length 268;
Best Local Similarity 87.5%; Pred. No. 7.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HQYLSST 8
Db 244 HQYLSST 251

RESULT 15
AAW90224
ID AAW90224 standard; Protein; 273 AA.
XX
XX AAW90224;
XX
XX 10-MAY-1999 (first entry)
XX
XX Anti-B7.1/anti-B7.2 bispecific diabody II.
XX
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX CD86; T cell activation; inhibitor; graft versus host disease;
XX transplant rejection; allograft rejection; autoimmune disease;
XX allergy; therapy; human; diabody; antibody; B7-24; 1G10.
XX Chimeric - Mus sp.
XX Chimeric - synthetic.
XX Key Location/Qualifiers
XX Peptide 1..39
XX Region 40..155
XX Peptide /note= "anti B7.1 Mab VH region"
XX Region 156..160
XX Peptide /note= "G4S flexible linker"
XX Region 161..273
XX Misc-difference 21
XX /note= "anti B7.2 Mab VL region"
XX /note= "encoded by TCA"
XX WO9858965-A2.
XX 30-DEC-1998.
XX 22-JUN-1998; 98WO-EP03791.
XX 20-JUN-1997; 97EP-0870092.
XX (INNO-) INNOGENETICS NV.
XX Bosman A, Buyse M, Lorre K, Sablon E;
XX WPI: 1999-105615/09.
XX N-PSDB: AAX01656.
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX immune diseases including allograft rejection
XX Example 7.2; Fig 30; 182pp; English.
XX This polypeptide comprises a bispecific diabody composed of the VH
XX region of anti-B7.1 monoclonal antibody (Mab) B7-24 joined via a
XX short, flexible linker to the VL region of anti-B7.2 Mab 1G10.
XX Mono- or bispecific bivalent molecules are generated by shortening
XX the flexible linker sequence between the VH and VL of the anti-B7.1
XX scFv B7-24, the anti-B7.2 scFv 1G10 and the scFv molecule with
XX dual specificity for B7.1 and B7.2 (B7.12) to 5-10 residues, and
XX for bispecific molecules by cross-pairing the VH and VL domains
XX from the 2 scFvs with different antigen recognition (B7.1/B7.2 and
XX B7.12/B7.12). The invention relates to novel molecules, including
XX diabodies, which can cross-link and/or cross-react with the
XX costimulatory molecules B7.1 and B7.2 expressed on professional
XX antigen-presenting cells, leading to the inhibition of antigen-
XX specific T cell activation. Methods are provided for the
XX production of such B7-binding molecules, and for their use in the
XX treatment or prevention of diseases of the immune system, in
XX particular graft rejection, graft versus host disease, allergy and
XX autoimmune diseases (claimed).
XX Sequence 273 AA;

Query Match 88.6%; Score 39; DB 20; Length 273;
Best Local Similarity 87.5%; Pred. No. 7.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
Db 255 HQYLSSWT 262

Search completed: August 13, 2003, 09:45:14
Job time : 85 secs

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OM protein - protein search, using sw model

Run on: August 13, 2003, 09:18:10 ; Search time 16 Seconds
(without alignments)
21.155 Million cell updates/sec

Title: US-10-056-052A-29
Perfect score: 44
Sequence: 1 HQYLSSVT 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

al number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 39 | 88.6 | 112 | 4 | US-08-435-516-4 |
| 2 | 39 | 88.6 | 112 | 4 | US-08-435-516-28 |
| 3 | 39 | 88.6 | 113 | 1 | US-08-690-102A-2 |
| 4 | 39 | 88.6 | 113 | 1 | US-08-690-102A-6 |
| 5 | 39 | 88.6 | 113 | 3 | US-09-127-902-2 |
| 6 | 39 | 88.6 | 113 | 3 | US-09-127-902-6 |
| 7 | 39 | 88.6 | 113 | 3 | US-09-155-107-2 |
| 8 | 39 | 88.6 | 113 | 3 | US-09-155-107-6 |
| 9 | 39 | 88.6 | 113 | 3 | US-09-155-107-20 |
| 10 | 39 | 88.6 | 113 | 5 | PCT-US95-09641-2 |
| 11 | 39 | 88.6 | 113 | 5 | PCT-US95-09641-6 |
| 12 | 39 | 88.6 | 301 | 2 | US-08-661-052-14 |
| 13 | 39 | 88.6 | 301 | 3 | US-09-188-082-14 |
| 14 | 39 | 88.6 | 301 | 4 | US-09-364-088-14 |
| 15 | 39 | 88.6 | 301 | 4 | US-09-102-716-14 |
| 16 | 39 | 88.6 | 553 | 2 | US-08-661-052-16 |
| 17 | 39 | 88.6 | 553 | 3 | US-09-188-082-16 |
| 18 | 39 | 88.6 | 553 | 4 | US-09-364-088-16 |
| 19 | 39 | 88.6 | 553 | 4 | US-09-102-716-16 |
| 20 | 33 | 75.0 | 554 | 2 | US-08-524-051-2 |
| 21 | 33 | 75.0 | 554 | 3 | US-09-052-778-16 |
| 22 | 33 | 75.0 | 902 | 4 | US-09-699-266A-12 |
| 23 | 33 | 75.0 | 921 | 4 | US-09-699-266A-9 |
| 24 | 32 | 72.7 | 87 | 4 | US-09-328-352-7319 |
| 25 | 31 | 70.5 | 313 | 4 | US-09-328-352-7621 |
| 26 | 31 | 70.5 | 390 | 4 | US-09-134-001C-3112 |
| 27 | 31 | 70.5 | 588 | 1 | US-07-903-466-3 |

| | | | | | | |
|----|----|------|-----|---|----------------------|--------------------|
| 28 | 31 | 70.5 | 588 | 5 | PCT-US93-05794-3 | Sequence 3, Appli |
| 29 | 30 | 68.2 | 162 | 4 | US-09-522-217-2 | Sequence 2, Appli |
| 30 | 30 | 68.2 | 308 | 4 | US-09-252-991A-20925 | Sequence 20925, A |
| 31 | 30 | 68.2 | 357 | 4 | US-09-574-942-4 | Sequence 4, Appli |
| 32 | 30 | 68.2 | 414 | 1 | US-08-235-471-9 | Sequence 9, Appli |
| 33 | 30 | 68.2 | 459 | 3 | US-09-071-709-1 | Sequence 1, Appli |
| 34 | 30 | 68.2 | 519 | 4 | US-09-522-217-85 | Sequence 85, Appli |
| 35 | 30 | 68.2 | 655 | 4 | US-09-245-808-1 | Sequence 1, Appli |
| 36 | 30 | 68.2 | 655 | 4 | US-09-767-594-1 | Sequence 1, Appli |
| 37 | 30 | 68.2 | 667 | 3 | US-09-071-709-9 | Sequence 9, Appli |
| 38 | 30 | 68.2 | 814 | 4 | US-09-107-532A-5510 | Sequence 5510, Ap |
| 39 | 30 | 68.2 | 829 | 4 | US-09-252-991A-27150 | Sequence 27150, A |
| 40 | 30 | 68.2 | 873 | 3 | US-09-187-331-6 | Sequence 6, Appli |
| 41 | 30 | 68.2 | 873 | 4 | US-09-470-946-6 | Sequence 6, Appli |
| 42 | 30 | 68.2 | 873 | 4 | US-09-438-906-2 | Sequence 2, Appli |
| 43 | 30 | 68.2 | 873 | 4 | US-09-438-906-4 | Sequence 4, Appli |
| 44 | 30 | 68.2 | 925 | 2 | US-08-392-946-1 | Sequence 1, Appli |
| 45 | 30 | 68.2 | 925 | 2 | US-08-504-169-1 | Sequence 1, Appli |

ALIGNMENTS

RESULT 1
US-08-435-516-4
; Sequence 4, Application US/08435516
; Patent No. 6500931
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
; TITLE OF INVENTION: IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384
; FILING DATE: 04-NOV-1992; -02-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
US-08-435-516-4

Query Match 88.6%; Score 39; DB 4; Length 112;
Best Local Similarity 87.5%; Pred. No. 0.92;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HQYLSSVT 8
Db 95 HQYLSSWT 102

RESULT 2
US-08-435-516-28
; Sequence 28, Application US/08435516

Patent No. 6500931
GENERAL INFORMATION:
APPLICANT: NAME: SAXE, Bernhard D.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
NUMBER OF SEQUENCES: 28 TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,516
FILING DATE: 01-JUL-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384
FILING DATE: 04-NOV-1992; 02-NOV-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-435-516-28

Query Match 88.6%; Score 39; DB 4; Length 112;
Best Local Similarity 87.5%; Pred. No. 0.92;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
DB 95 HQYLSSWT 102

RESULT 3
US-08-690-102A-2
Sequence 2, Application US/08690102A
Patent No. 5789554
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,102A
FILING DATE: 01-JUL-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-690-102A-6

Query Match 88.6%; Score 39; DB 1; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
DB 95 HQYLSSWT 102

RESULT 4
US-08-690-102A-6
Sequence 6, Application US/08690102A
Patent No. 5789554
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,102A
FILING DATE: 01-JUL-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-690-102A-6

Query Match 88.6%; Score 39; DB 1; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
DB 95 HQYLSSWT 102

NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-690-102A-2

Query Match 88.6%; Score 39; DB 1; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
DB 95 HQYLSSWT 102

RESULT 4
US-08-690-102A-6
Sequence 6, Application US/08690102A
Patent No. 5789554
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,102A
FILING DATE: 01-JUL-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-690-102A-6

Query Match 88.6%; Score 39; DB 1; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
DB 95 HQYLSSWT 102

Db 95 HOYLSSWT 102

RESULT 5

US-09-127-902-2
; Sequence 2, Application US/09127902
; Patent No. 6187287
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/127,902
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/690,102
; FILING DATE: 01-JUL-1996
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; -09-127-902-2

Query Match 88.6%; Score 39; DB 3; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYLSSYT 8
Db 95 HOYLSSWT 102

RESULT 6

US-09-127-902-6
; Sequence 6, Application US/09127902
; Patent No. 6187287
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.

COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/127,902
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/690,102
; FILING DATE: 01-JUL-1996
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136

INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-127-902-6

Query Match 88.6%; Score 39; DB 3; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYLSSYT 8
Db 95 HOYLSSWT 102

RESULT 7

US-09-155-107-2
; Sequence 2, Application US/09155107
; Patent No. 6254868
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/0879
; CURRENT APPLICATION NUMBER: US/09/155,107
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: US 60/013,709
; EARLIER FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
; US-09-155-107-2

Qy 1 HOYLSSYT 8
Db 95 HOYLSSWT 102

Query Match 88.6%; Score 39; DB 3; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
US-09-155-107-6
; Sequence 6, Application US/09155107
; Patent No. 6254868
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/0879
; CURRENT APPLICATION NUMBER: US/09/155.107
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: US 60/013.709
; EARLIER FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-155-107-6

Query Match 88.6%; Score 39; DB 3; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1-HQYLSSYT 8
Db 95 HQYLSSWT 102

RESULT 9
US-09-155-107-20
; Sequence 20, Application US/09155107
; Patent No. 6254868
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/0879
; CURRENT APPLICATION NUMBER: US/09/155.107
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: US 60/013.709
; EARLIER FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-155-107-20

Query Match 88.6%; Score 39; DB 3; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
Db 95 HQYLSSWT 102

RESULT 10
PCT-US95-09641-2
; Sequence 2, Application PC/TUS9509641
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09641
; FILING DATE: 11-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-09641-2

Query Match 88.6%; Score 39; DB 5; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
Db 95 HQYLSSWT 102

RESULT 11
PCT-US95-09641-6
; Sequence 6, Application PC/TUS9509641
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; NUMBER OF SEQUENCES: 21
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09641
; FILING DATE: 11-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-09641-6

Query Match 88.6%; Score 39; DB 5; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
Db 95 HQYLSSWT 102

RESULT 12
US-08-661-052-14
; Sequence 14, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: yashwant M. Deo
; APPLICANT: Joel Goldstein

APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-661-052-14

Query Match 88.6%; Score 39; DB 2; Length 301;
Best Local Similarity 87.5%; Pred. No. 2.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSSYT 8
Db 249 HOYLSSWT 256

RESULT 13
US-09-188-082-14
Sequence 14, Application US/09188082
Patent No. 6270765
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/188,082
FILING DATE: 07-JUNE-1996
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane E.
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: MXI-043CP2
TELEPHONE: (617)227-7400
TELEFAX: (617)742-7414
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-188-082-14

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-188-082-14

Query Match 88.6%; Score 39; DB 3; Length 301;
Best Local Similarity 87.5%; Pred. No. 2.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSSYT 8
Db 249 HOYLSSWT 256

RESULT 14
US-09-364-088-14
Sequence 14, Application US/09364088
Patent No. 6365161
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo, et al.
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street, 24th Floor
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,088
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/188,082
FILING DATE: 07-JUNE-1996
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane E.
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: MXI-043CP2
TELEPHONE: (617)227-7400
TELEFAX: (617)742-7414
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-364-088-14

Query Match 88.6%; Score 39; DB 4; Length 301;
Best Local Similarity 87.5%; Pred. No. 2.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8

Db 249 HQYLSSWT 256

RESULT 15

US-09-102-716-14
; Sequence 14, Application US/09102716
; Patent No. 6395272
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; Joel Goldstein
; Robert Graziano
; Chезian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,716
; FILING DATE: 22-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-102-716-14

Query Match 88.6%; Score 39; DB 4; Length 301;
Best Local Similarity 87.5%; Pred. No. 2.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8

Db 249 HQYLSSWT 256

Search completed: August 13, 2003, 09:39:56
Job time : 17 secs

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OM protein - protein search, using sw model

Run on: August 13, 2003, 09:37:35 ; Search time 24 Seconds
(without alignments)
43.668 Million cell updates/sec

Title: US-10-056-052A-29

Perfect score: 44

Sequence: 1 HQYLSSYT 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

al number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description |
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| 1 | 44 | 100.0 | 112 | 15 | US-10-056-052-10 |
| 2 | 44 | 100.0 | 112 | 15 | US-10-056-052-14 |
| 3 | 44 | 100.0 | 112 | 15 | US-10-056-052-18 |
| 4 | 39 | 88.6 | 112 | 12 | US-10-229-335-4 |
| 5 | 39 | 88.6 | 112 | 12 | US-10-229-335-28 |
| 6 | 39 | 88.6 | 112 | 15 | US-10-056-052-6 |
| 7 | 39 | 88.6 | 113 | 10 | US-09-741-843-2 |
| 8 | 39 | 88.6 | 113 | 10 | US-09-741-843-6 |
| 9 | 39 | 88.6 | 113 | 11 | US-09-894-839-2 |
| 10 | 39 | 88.6 | 113 | 11 | US-09-894-839-6 |
| 11 | 39 | 88.6 | 113 | 11 | US-09-894-839-20 |
| 12 | 39 | 88.6 | 113 | 11 | US-09-988-013A-2 |
| 13 | 39 | 88.6 | 113 | 11 | US-09-988-013A-6 |
| 14 | 35 | 79.5 | 272 | 12 | US-10-053-530-14 |
| 15 | 35 | 79.5 | 272 | 15 | US-10-207-655-14 |

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| 16 | 33 | 75.0 | 902 | 15 | US-10-231-778-222 | Sequence 222, App |
| 17 | 33 | 75.0 | 931 | 10 | US-09-906-453-2 | Sequence 2, Appli |
| 18 | 32 | 72.7 | 235 | 9 | US-09-815-242-5455 | Sequence 5455, Ap |
| 19 | 32 | 72.7 | 235 | 9 | US-09-815-242-12684 | Sequence 12684, A |
| 20 | 32 | 72.7 | 272 | 11 | US-09-774-639-167 | Sequence 167, App |
| 21 | 32 | 72.7 | 272 | 11 | US-09-969-730-120 | Sequence 120, App |
| 22 | 31 | 70.5 | 368 | 15 | US-10-205-823-377 | Sequence 377, App |
| 23 | 31 | 70.5 | 399 | 9 | US-09-925-301-1385 | Sequence 1385, Ap |
| 24 | 31 | 70.5 | 588 | 10 | US-09-908-193-34 | Sequence 34, Appl |
| 25 | 31 | 70.5 | 588 | 12 | US-10-301-822-213 | Sequence 213, App |
| 26 | 31 | 70.5 | 695 | 9 | US-09-764-898-191 | Sequence 191, App |
| 27 | 31 | 70.5 | 754 | 10 | US-09-908-193-32 | Sequence 32, Appl |
| 28 | 31 | 70.5 | 776 | 10 | US-09-908-193-33 | Sequence 33, Appl |
| 29 | 31 | 70.5 | 778 | 10 | US-09-908-193-8 | Sequence 8, Appli |
| 30 | 31 | 70.5 | 779 | 10 | US-09-908-193-10 | Sequence 10, Appl |
| 31 | 30 | 68.2 | 12 | 10 | US-09-982-172-201 | Sequence 201, App |
| 32 | 30 | 68.2 | 12 | 10 | US-09-982-172-249 | Sequence 249, App |
| 33 | 30 | 68.2 | 62 | 9 | US-09-864-761-43345 | Sequence 43345, A |
| 34 | 30 | 68.2 | 162 | 10 | US-09-923-246-2 | Sequence 2, Appli |
| 35 | 30 | 68.2 | 162 | 10 | US-09-925-561A-10 | Sequence 10, Appl |
| 36 | 30 | 68.2 | 162 | 11 | US-09-972-218A-19 | Sequence 19, Appl |
| 37 | 30 | 68.2 | 162 | 12 | US-10-282-622-2 | Sequence 2, Appli |
| 38 | 30 | 68.2 | 162 | 12 | US-10-282-622-6 | Sequence 6, Appli |
| 39 | 30 | 68.2 | 162 | 15 | US-10-264-634-19 | Sequence 19, Appl |
| 40 | 30 | 68.2 | 162 | 15 | US-10-295-723-2 | Sequence 2, Appli |
| 41 | 30 | 68.2 | 252 | 9 | US-09-925-299-925 | Sequence 925, App |
| 42 | 30 | 68.2 | 252 | 11 | US-09-925-299-925 | Sequence 925, App |
| 43 | 30 | 68.2 | 357 | 9 | US-09-949-434-4 | Sequence 4, Appli |
| 44 | 30 | 68.2 | 483 | 10 | US-09-881-752A-354 | Sequence 354, App |
| 45 | 30 | 68.2 | 519 | 10 | US-09-923-246-85 | Sequence 85, Appl |

ALIGNMENTS

RESULT 1
US-10-056-052-10
; Sequence 10, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-10

Query Match 100.0%; Score 44; DB 15; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8

Db 95 HQYLSSYT 102

```
RESULT 2
US-10-056-052-14
; Sequence 14, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056.052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-14

Query Match      100.0%; Score 44; DB 15; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HOYLSSYT 8
Db      95 HOYLSSYT 102

RESULT 3
US-10-056-052-18
; Sequence 18, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056.052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-18

Query Match      100.0%; Score 44; DB 15; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HOYLSSYT 8
Db      95 HOYLSSYT 102

RESULT 4
US-10-229-335-4
; Sequence 4, Application US/10229335
; Publication No. US20030144483A1
; GENERAL INFORMATION:
; APPLICANT: MEDAREX, INC.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
; IMMUNOBLOBLIN G ON HUMAN MONONUCLEAR PHAGOCYTES
; NUMBER OF SEQUENCES: 28
; STREET: P.O. Box 953, 1545 Route 22 East
; CITY: Annandale
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/229,335
; FILING DATE: 26-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,516
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-229-335-4

Query Match      88.6%; Score 39; DB 12; Length 112;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HOYLSSYT 8
Db      95 HOYLSSWT 102

RESULT 5
US-10-229-335-28
; Sequence 28, Application US/10229335
; Publication No. US20030144483A1
; GENERAL INFORMATION:
; APPLICANT: MEDAREX, INC.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
; IMMUNOBLOBLIN G ON HUMAN MONONUCLEAR PHAGOCYTES
; NUMBER OF SEQUENCES: 28
; STREET: P.O. Box 953, 1545 Route 22 East
; CITY: Annandale
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08801
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,335
FILING DATE: 26-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/435,516
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-229-335-28

Query Match 88.6%; Score 39; DB 12; Length 112;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|||||:|
Db 95 HQYLSSWT 102

RESULT 6
US-10-056-052-6
Sequence 6, Application US/10056052
Publication No. US20030099656A1
GENERAL INFORMATION:
APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: HALL, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN
FILE REFERENCE: P07069US04/BAS
CURRENT APPLICATION NUMBER: US/10/056,052
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/298,413
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/274,611
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/264,072
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 112
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-056-052-6

Query Match 88.6%; Score 39; DB 15; Length 112;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|||||:|

Db 95 HQYLSSWT 102
RESULT 7
US-09-741-843-2
Sequence 2, Application US/09741843
Patent No. US20020102254A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL
TITLE OF INVENTION: AND LEUKEMIA CELLS
FILE REFERENCE: 018733/0996
CURRENT APPLICATION NUMBER: US/09/741,843
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/127,902
PRIOR FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 08/690,102
PRIOR FILING DATE: 1996-07-06
PRIOR APPLICATION NUMBER: US 08/289,576
PRIOR FILING DATE: 1994-08-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 113
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-741-843-2

Query Match 88.6%; Score 39; DB 10; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|||||:|
Db 95 HQYLSSWT 102

RESULT 8
US-09-741-843-6
Sequence 6, Application US/09741843
Patent No. US20020102254A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL
TITLE OF INVENTION: AND LEUKEMIA CELLS
FILE REFERENCE: 018733/0996
CURRENT APPLICATION NUMBER: US/09/741,843
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/127,902
PRIOR FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 08/690,102
PRIOR FILING DATE: 1996-07-06
PRIOR APPLICATION NUMBER: US 08/289,576
PRIOR FILING DATE: 1994-08-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-09-741-843-6

Query Match 88.6%; Score 39; DB 10; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|||||:|
Db 95 HQYLSSWT 102

RESULT 9
US-09-894-839-2
; Sequence 2, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: OU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-894-839-2

Query Match 88.6%; Score 39; DB 11; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYLSSYT 8
Db 95 HOYLSSWT 102

RESULT 10
US-09-894-839-6
; Sequence 6, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: OU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-894-839-6

Query Match 88.6%; Score 39; DB 11; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYLSSYT 8
Db 95 HOYLSSWT 102

RESULT 11
US-09-894-839-20
; Sequence 20, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans

; APPLICANT: OU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-894-839-20

Query Match 88.6%; Score 39; DB 11; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYLSSYT 8
Db 95 HOYLSSWT 102

RESULT 12
US-09-988-013A-2
; Sequence 2, Application US/09988013A
; Publication No. US20030103979A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
; FILE REFERENCE: 18733/1082
; CURRENT APPLICATION NUMBER: US/09/988,013A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 09/741,843
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-988-013A-2

Query Match 88.6%; Score 39; DB 11; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYLSSYT 8
Db 95 HOYLSSWT 102

RESULT 13
US-09-988-013A-6
; Sequence 6, Application US/09988013A
; Publication No. US20030103979A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
; FILE REFERENCE: 18733/1082

; CURRENT APPLICATION NUMBER: US/09/988.013A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 09/741,843
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-988-013A-6

Query Match 88.6%; Score 39; DB 11; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|||||:|
Db 95 HQYLSSWT 102

RESULT 14

US-10-053-530-14
; Sequence 14, Application US/10053530
; Publication No. US2003013939A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey
; APPLICANT: Hayden-Ledbetter, Martha
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 390069.401
; CURRENT APPLICATION NUMBER: US/10/053,530
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 09/765,208
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
LOCATION: (1)..(272)
OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-10-053-530-14

Query Match 79.5%; Score 35; DB 12; Length 272;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|||||:|
Db 115 HQFLSSWT 122

RESULT 15

US-10-207-655-14
; Sequence 14, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
LOCATION: (1)..(272)
OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-10-207-655-14

Query Match 79.5%; Score 35; DB 15; Length 272;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|||||:|
Db 115 HQFLSSWT 122

Search completed: August 13, 2003, 09:43:43
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw_model

Run on: August 13, 2003, 09:43:16 ; Search time 38 seconds
(without alignments)
20.246 Million cell updates/sec

Title: US-10-056-052A-29
Perfect score: 44
Sequence: 1 HQYLSSYT 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 44 | 100.0 | 103 | 2 PH1054 | Ig light chain V r |
| 2 | 37 | 84.1 | 101 | 2 S26337 | Ig light chain V r |
| 3 | 34 | 77.3 | 88 | 2 C82627 | hypothetical prote |
| 4 | 34 | 77.3 | 468 | 2 E81924 | probable two-compo |
| 5 | 34 | 77.3 | 543 | 2 A32693 | steroid receptor p |
| 6 | 34 | 77.3 | 746 | 2 B32693 | steroid receptor p |
| 7 | 34 | 77.3 | 1226 | 2 H64479 | protoporphyrin IX |
| 8 | 34 | 77.3 | 1481 | 2 S78373 | DNA-directed RNA p |
| 9 | 34 | 77.3 | 2531 | 2 T31070 | notch homolog - se |
| 10 | 33 | 75.0 | 113 | 2 S66936 | probable membrane |
| 11 | 33 | 75.0 | 462 | 2 C81701 | hypothetical prote |
| 12 | 33 | 75.0 | 554 | 2 A56596 | chitinase (EC 3.2. |
| 13 | 33 | 75.0 | 730 | 2 T16455 | hypothetical prote |
| 14 | 33 | 75.0 | 796 | 2 AG1849 | serine/threonine k |
| 15 | 33 | 75.0 | 902 | 2 T01127 | curly leaf protein |
| 16 | 32 | 72.7 | 215 | 1 SXADWS | hexon-associated p |
| 17 | 32 | 72.7 | 226 | 2 D90034 | glucanate operon t |
| 18 | 32 | 72.7 | 245 | 2 D71554 | probable adenylate |
| 19 | 32 | 72.7 | 294 | 2 AF1218 | Salmonella typhimu |
| 20 | 32 | 72.7 | 294 | 2 A11571 | regulatory protein |
| 21 | 32 | 72.7 | 586 | 2 JC6500 | hnf-3/forkhead tra |
| 22 | 32 | 72.7 | 610 | 2 C96732 | hypothetical prote |
| 23 | 32 | 72.7 | 663 | 2 T40493 | hnf-3/forkhead tra |
| 24 | 32 | 72.7 | 1086 | 2 T40354 | hypothetical prote |
| 25 | 32 | 72.7 | 1628 | 2 T38055 | hypothetical prote |
| 26 | 31 | 70.5 | 138 | 2 T21299 | hypothetical prote |
| 27 | 31 | 70.5 | 149 | 2 D84181 | hypothetical prote |
| 28 | 31 | 70.5 | 218 | 2 D64227 | major sigma factor |
| 29 | 31 | 70.5 | 234 | 2 T24374 | hypothetical prote |

| | | | | | |
|----|----|------|------|----------|--------------------|
| 30 | 31 | 70.5 | 297 | 2 D83825 | hypothetical prote |
| 31 | 31 | 70.5 | 341 | 2 T16951 | hypothetical prote |
| 32 | 31 | 70.5 | 368 | 2 S54160 | spermine synthase |
| 33 | 31 | 70.5 | 410 | 2 S28485 | lipopolysaccharide |
| 34 | 31 | 70.5 | 506 | 2 T07209 | H+-transporting tw |
| 35 | 31 | 70.5 | 553 | 2 T40438 | hypothetical prote |
| 36 | 31 | 70.5 | 588 | 2 A49618 | probable ataxia-te |
| 37 | 31 | 70.5 | 620 | 2 E82351 | ATP-dependent DNA |
| 38 | 31 | 70.5 | 776 | 2 S28258 | androgen-regulated |
| 39 | 31 | 70.5 | 1148 | 2 T18770 | probable calcium c |
| 40 | 31 | 70.5 | 1279 | 2 T17194 | protoporphyrin IX |
| 41 | 31 | 70.5 | 4436 | 2 E71086 | hypothetical prote |
| 42 | 30 | 68.2 | 103 | 2 G42528 | B26R protein - vac |
| 43 | 30 | 68.2 | 111 | 2 G30502 | Ig kappa chain V r |
| 44 | 30 | 68.2 | 161 | 2 E84201 | hypothetical prote |
| 45 | 30 | 68.2 | 204 | 2 T25709 | hypothetical prote |

ALIGNMENTS

RESULT 1

PH1054
Ig light chain V region (clone 202.135) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1054
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1054
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-103 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 44; DB 2; Length:103;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
Db 95 HQYLSSYT 102

RESULT 2

S26337
Ig light chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C:Accession: S26337; S78449
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protei
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26337
A:Molecule type: mRNA
A:Residues: 1-101 <STA>
A:Cross-references: EMBL:X59193
R:Caton, A.J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S78447
A:Accession: S78449
A:Molecule type: mRNA
A:Residues: 1-60, '62-91, '93-101 <CAT>
A:Cross-references: EMBL:X59193; NID:G52323; PIDN:CAA41903.1; PID:G1334067
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-88/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 37; DB 2; Length 101;
 Best Local Similarity 75.0%; Pred. No. 1.5;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSSYT 8
 |||||:|
 Db 87 HOYLSTFT 94

RESULT 3
 C82627
 hypothetical protein XF1883 [imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: C82627
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717; PMID:10910347
 Note: for a complete list of authors see reference number A59328 below
 A:Accession: C82627
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-88 <SIM>
 A:Cross-references: GB:AE003849; NID:g9106961; PIDN:AAF84689.1; GSPDB:GN001
 A:Experimental source: strain 9a5c
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laio
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tshuako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovsky-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF1883

Query Match 77.3%; Score 34; DB 2; Length 88;
 Best Local Similarity 75.0%; Pred. No. 5.6;
 Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 HOYLSSYT 8
 |||||:|
 Db 15 HOYISSLT 22

RESULT 4
 E81924
 probable two-component system sensor kinase (EC 2.7.3.-) NMA0797 [imported] - Neisseria
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: E81924
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 ; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.
 A:Reference number: A81775; MUID:20222556; PMID:10761919
 A:Accession: E81924
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-468 <PAR>
 A:Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84080.1; PID:g737951
 A:Experimental source: serogroup A, strain 22491
 C:Genetics:
 A:Gene: NMA0797
 C:Keywords: phosphotransferase

Query Match 77.3%; Score 34; DB 2; Length 468;
 Best Local Similarity 62.5%; Pred. No. 33;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSSYT 8
 |||||:|
 Db 93 HRVIDSYT 100

RESULT 5
 A32693
 steroid receptor protein svp 1 - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
 C:Accession: A32693
 R:Midzvik, M.; Hiromi, Y.; Weber, U.; Goodman, C.S.; Rubin, G.M.
 Cell 60, 211-224, 1990
 A:Title: The Drosophila seven-up gene, a member of the steroid receptor gene superfam
 A:Reference number: A32693; MUID:90124631; PMID:2105166
 A:Accession: A32693
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-543 <MLO>
 A:Cross-references: GB:M28863; NID:g158518; PIDN:AAA62770.1; PID:g158519
 C:Genetics:
 A:Gene: FlyBase:svp
 A:Cross-references: FlyBase:FBgn0003651
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: alternative splicing; DNA binding; steroid hormone receptor; transcriptio
 F:198-452/Domain: erba transforming protein homology <ERBA>
 F:200-220/Region: zinc finger
 F:236-260/Region: zinc finger

Query Match 77.3%; Score 34; DB 2; Length 543;
 Best Local Similarity 85.7%; Pred. No. 39;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSSYT 7
 |||||:
 Db 305 HSYLSSYT 311

RESULT 6
 B32693
 steroid receptor protein svp 2 - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 12-Sep-1997
 C:Accession: B32693
 R:Midzvik, M.; Hiromi, Y.; Weber, U.; Goodman, C.S.; Rubin, G.M.
 Cell 60, 211-224, 1990
 A:Title: The Drosophila seven-up gene, a member of the steroid receptor gene superfam
 A:Reference number: A32693; MUID:90124631; PMID:2105166
 A:Accession: B32693
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-746 <MLO>
 A:Cross-references: GB:M28863; GB:M28864
 C:Genetics:
 A:Gene: FlyBase:svp
 A:Cross-references: FlyBase:FBgn0003651
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: alternative splicing; DNA binding; steroid hormone receptor; transcriptio
 F:198-452/Domain: erba transforming protein homology <ERBA>
 F:200-220/Region: zinc finger
 F:236-260/Region: zinc finger

Query Match 77.3%; Score 34; DB 2; Length 746;
 Best Local Similarity 85.7%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSSYT 7
 |||||:

Db 305 HSYLSSY 311

RESULT 7

H64479

protoporphyrin IX magnesium chelatase (EC 4.99.1.-) homolog - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Oct-1999
C:Accession: H64479
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Raon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: H64479
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
Residues: 1-1226 <BUL>
C:Cross-references: GB:U67585; GB:L77117; NID:g1592088; PIDN:AAB99452.1; PID:g1500323; T Genetics:
A:Map position: FOR1408283-1411963
C:Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
C:Keywords: lyase

Query Match 77.3%; Score 34; DB 2; Length 1226;

Best Local Similarity 71.4%; Pred. No. 92;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYLSSY 7

|||||

Db 509 HOYIASY 515

RESULT 8

S78373

DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - Odontella sinensis chloroplast
C:Species: Chloroplast Odontella sinensis
C:Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 20-Jun-2000
C:Accession: S78373
R:Kowalik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
Plant Mol. Biol. Rep. 13, 336-342, 1995
A:Title: The Chloroplast Genome of a chlorophyll a+c containing Alga, Odontella sinensis
A:Reference number: S78238
A:Accession: S78373
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
Residues: 1-1481 <KOW>

C:Cross-references: EMBL:Z67753; NID:g1185127; PID:g1185263

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995

C:Genetics:

A:Gene: rpoC2

A:Genome: chloroplast

C:Superfamily: chloroplast DNA-directed RNA polymerase beta'-2 chain

C:Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 77.3%; Score 34; DB 2; Length 1481;

Best Local Similarity 62.5%; Pred. No. 1.1e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSSY 8

|||||

Db 924 HOFIDSYT 931

RESULT 9

T31070

notch homolog - sea urchin (Lytechinus variegatus)
C:Species: Lytechinus variegatus (variegated urchin)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C:Accession: T31070
R:Sherwood, D.R.; McClay, D.R.

Development 124, 3363-3374, 1997

A:Title: Identification and localization of a sea urchin Notch homologue: insights in
A:Reference number: Z20966; MUID:97454256; PMID:9310331

A:Accession: T31070

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2531 <SHE>

A:Cross-references: EMBL:AF000634; NID:g2570350; PID:g2570351; PIDN:AAB82088.1

C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 77.3%; Score 34; DB 2; Length 2531;

Best Local Similarity 62.5%; Pred. No. 2e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSSY 8

|||||

Db 949 HEYVDSY 956

RESULT 10

S66936

probable membrane protein YOR053w - yeast (Saccharomyces cerevisiae)

A:Alternate names: hypothetical protein O2799

C:Species: Saccharomyces cerevisiae

C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002

C:Accession: S66936; S66927

R:Bohn, C.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Dang, D.V.; Valens, M.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S66929

A:Accession: S66936

A:Molecule type: DNA

A:Residues: 1-113 <BOH>

A:Cross-references: EMBL:Z74961; NID:g1420189; PID:e252336; PID:g1420189; MIPS:YOR053

A:Experimental source: strain S288C

R:Landt, O.; Hiesel, R.; Unseld, M.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S66907

A:Accession: S66927

A:Molecule type: DNA

A:Residues: 1-8 <LAN>

A:Cross-references: EMBL:Z74961; MIPS:YOR053w

A:Experimental source: strain S288C

C:Genetics:

A:Map position: 15R

C:Keywords: transmembrane protein

F:3-19/Domain: transmembrane #status predicted <TMM>

Query Match 75.0%; Score 33; DB 2; Length 113;

Best Local Similarity 85.7%; Pred. No. 12;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLSSY 7

|||||

Db 82 HOYRSSY 88

RESULT 11

C81701

hypothetical protein TC0441 [imported] - Chlamydia muridarum (strain N19g)

C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000

C:Accession: C81701

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke

, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolony, J.; McClarty, G.; Salzbe

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39

A:Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: C81701

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-462 <TET>

A:Cross-references: GB:AE002313; GB:AE002160; NID:g7190484; PIDN:AAF39295.1; PID:g719

A:Experimental source: strain Nigg (MoPn)
C:Genetics:
A:Gene: TC0441

Query Match 75.0%; Score 33; DB 2; Length 462;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSSY 7
|:|||||
DB 440 HEYLSTY 446

RESULT 12

A:Accession: A56596
C:Species: Manduca sexta (tobacco hornworm)
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 29-Jan-1999
C:Accession: A56596
A:Title: Sequence of a cDNA and expression of the gene encoding epidermal and gut chitinase (EC 3.2.1.14) - tobacco hornworm
A:Reference number: A56596; MUID:93357793; PMID:833525
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-554 <KRA>
A:Cross-references: GB:U02270; GB:S64757; NID:9406048; PID:9406049
A:Experimental source: larvae
A:Note: sequence extracted from NCBI backbone (NCBIN:136417, NCBI:136418)
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 75.0%; Score 33; DB 2; Length 554;
Best Local Similarity 62.5%; Pred. No. 64;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSSYT 8
|:|||||
DB 392 HKHMSSYT 399

RESULT 13

A:Accession: T16455
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16455
A:Title: Hypothetical protein F55D10.3 - Caenorhabditis elegans
A:Reference number: Z18516
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-730 <LEI>
A:Cross-references: EMBL:U40948; NID:gl072223; PID:gl072224; PIDN:AAA81727.1; CESP:F55D10.3
A:Gene: CESP:F55D10.3
A:Introns: 48/3; 125/3; 181/3

Query Match 75.0%; Score 33; DB 2; Length 730;
Best Local Similarity 62.5%; Pred. No. 86;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSSYT 8
|:|||||
DB 430 HEYLKSYS 437

RESULT 14

A:Accession: AG1849
C:Species: Nostoc sp. (strain PCC 7120)
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AG1849
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Nostoc sp. PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG1849
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-796 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA072302.1; PID:gl7129689; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr0344

Query Match 75.0%; Score 33; DB 2; Length 796;
Best Local Similarity 71.4%; Pred. No. 94;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSSY 7
|:|||||
DB 147 HOYVTSY 153

RESULT 15

A:Accession: T01127
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 02-Feb-2001
C:Accession: T01127; A84624
A:Title: curly leaf protein (polycomb-group) [imported] - Arabidopsis thaliana
A:Reference number: Z14198
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-902 <ROU>
A:Cross-references: EMBL:AC003040; NID:g3242700; PID:g3242729
A:Experimental source: cultivar Columbia
A:Gene: At2g23380; F26B6.3
A:Introns: 21/3; 52/3; 153/2; 207/2; 235/3; 280/3; 296/3; 320/3; 554/2; 604/3; 679/2;

Search completed: August 13, 2003, 09:48:14
Job time : 41 secs

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OM protein - protein search, using sw model

Run on: August 13, 2003, 09:40:00 ; Search time 23.5 seconds
(without alignments)
16.357 Million cell updates/sec

Title: US-10-056-052A-29
Perfect score: 44
Sequence: 1 HQYLSSYT 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|------------|---------------------|
| 1 | 34 | 77.3 | 543 | 1 | 7UP1_DROME | P16375 drosophila |
| 2 | 34 | 77.3 | 746 | 1 | 7UP2_DROME | P16376 drosophila |
| 3 | 34 | 77.3 | 1481 | 1 | RPOD_ODOSI | P49468 odontella s |
| 4 | 33 | 75.0 | 554 | 1 | CHIT_MANSE | P36362 manduca sex |
| 5 | 33 | 75.0 | 902 | 1 | CLF_ARATH | P93831 arabidopsis |
| 6 | 32 | 72.7 | 215 | 1 | HEX8_ADEM1 | P19722 mouse adeno |
| 7 | 32 | 72.7 | 245 | 1 | KAD_CHLTR | O84130 chlamydia t |
| 8 | 32 | 72.7 | 663 | 1 | SEPI_SCHPO | O43058 schizosacch |
| 9 | 32 | 72.7 | 1628 | 1 | YATE_SCHPO | O09779 schizosacch |
| 10 | 31 | 70.5 | 218 | 1 | Y248_MYCGE | P47490 mycoplasma |
| 11 | 31 | 70.5 | 341 | 1 | YSX3_CAEEL | Q10022 caenorhabdi |
| 12 | 31 | 70.5 | 366 | 1 | SPSY_HUMAN | P52788 homo sapien |
| 13 | 31 | 70.5 | 366 | 1 | SPSY_MOUSE | P97355 mus musculu |
| 14 | 31 | 70.5 | 391 | 1 | CGAL_CARAU | Q92161 carassius a |
| 15 | 31 | 70.5 | 506 | 1 | ATPA_CHLVU | P56294 chlorella v |
| 16 | 31 | 70.5 | 553 | 1 | ME18_SCHPO | Q9ub29 schizosacch |
| 17 | 31 | 70.5 | 754 | 1 | AD07_HUMAN | Q9b2u9 homo sapien |
| 18 | 31 | 70.5 | 776 | 1 | AD07_MACFA | O28475 macaca fasc |
| 19 | 31 | 70.5 | 1279 | 1 | BCHH_CHLVU | O50314 chlorobium |
| 20 | 30 | 68.2 | 103 | 1 | V220_VACCC | P21104 vaccinia vi |
| 21 | 30 | 68.2 | 359 | 1 | MANR_PSEPU | P11444 pseudomonas |
| 22 | 30 | 68.2 | 377 | 1 | PKM1_CAEEL | Q17446 caenorhabdi |
| 23 | 30 | 68.2 | 410 | 1 | COT2_CHICK | Q90733 gallus gall |
| 24 | 30 | 68.2 | 414 | 1 | COT2_BOVIN | Q9ttr7 bos taurus |
| 25 | 30 | 68.2 | 414 | 1 | COT2_HUMAN | P24468 homo sapien |
| 26 | 30 | 68.2 | 414 | 1 | COT2_MOUSE | P43135 mus musculu |
| 27 | 30 | 68.2 | 414 | 1 | COT2_RAT | O09018 rattus norv |
| 28 | 30 | 68.2 | 444 | 1 | EX7L_RICCN | Q92qu6 rickettsia |
| 29 | 30 | 68.2 | 655 | 1 | ABG2_HUMAN | Q9unq0 homo sapien |
| 30 | 30 | 68.2 | 766 | 1 | PRTF_HSVBE | P28973 equine herp |
| 31 | 30 | 68.2 | 910 | 1 | HUL5_YEAST | P53119 saccharomyc |
| 32 | 30 | 68.2 | 925 | 1 | NPPI_HUMAN | P22413 h ectionucle |
| 33 | 30 | 68.2 | 1050 | 1 | BUIB_HUMAN | O60566 homo sapien |

RESULT 1
7UP1_DROME

| ID | 7UP1_DROME | STANDARD: | PRT: | 543 AA. |
|----|--|-----------|------|---------|
| AC | P16375; Q9VGB0; | | | |
| DT | 01-AUG-1990 (Rel. 15, Created) | | | |
| DT | 01-AUG-1990 (Rel. 15, Last sequence update) | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | |
| DE | Steroid receptor seven-up type 1. | | | |
| GN | SVP OR NR2F3 OR CG11502. | | | |
| OS | Drosophila melanogaster (Fruit fly). | | | |
| OC | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; | | | |
| OC | Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; | | | |
| OC | Ephydroidea; Drosophilidae; Drosophila. | | | |
| OX | NCBI_TaxID=7227; | | | |
| ON | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=90124631; PubMed=2105166; | | | |
| RA | Mlodzik M., Hironi Y., Weber U., Goodman C.S., Rubin G.M.; | | | |
| RT | "The drosophila seven-up gene, a member of the steroid receptor gene | | | |
| RL | superfamily, controls photoreceptor cell fates."; | | | |
| RL | Cell 60:211-224(1990). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=Berkley; | | | |
| RX | MEDLINE=20196006; PubMed=10731132; | | | |
| RA | Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D., | | | |
| RA | Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., | | | |
| RA | George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., | | | |
| RA | Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., | | | |
| RA | Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D., | | | |
| RA | Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., | | | |
| RA | April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., | | | |
| RA | Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., | | | |
| RA | Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., | | | |
| RA | Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P., | | | |
| RA | Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., | | | |
| RA | Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., | | | |
| RA | de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., | | | |
| RA | Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., | | | |
| RA | Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., | | | |
| RA | Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., | | | |
| RA | Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., | | | |
| RA | Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., | | | |
| RA | Hoskin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwuk C., | | | |
| RA | Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., | | | |
| RA | Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., | | | |
| RA | Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., | | | |
| RA | Liu X., Mattlei B., McIntosh T.C., McLeod M.P., McPherson D., | | | |
| RA | Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., | | | |
| RA | Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., | | | |
| RA | Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M., | | | |
| RA | Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., | | | |
| RA | Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., | | | |
| RA | Shue B.C., Stoen-Kiamos I., Simpson M., Skupski M.P., Smith T., | | | |
| RA | Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., | | | |
| RA | Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., | | | |

ALIGNMENTS

| | | | | | | |
|----|----|------|------|---|------------|--------------------|
| 34 | 30 | 68.2 | 1729 | 1 | RRP5_YEAST | Q05022 saccharomyc |
| 35 | 30 | 68.2 | 2703 | 1 | NOTC_DROME | P07207 drosophila |
| 36 | 29 | 65.9 | 104 | 1 | Y079_NPVP | O10332 orgyia pseu |
| 37 | 29 | 65.9 | 157 | 1 | ATPX_GALSU | P35012 galderia s |
| 38 | 29 | 65.9 | 230 | 1 | YD83_YEAST | Q04004 saccharomyc |
| 39 | 29 | 65.9 | 264 | 1 | Y061_UREPA | Q9pr84 ureaplasma |
| 40 | 29 | 65.9 | 285 | 1 | TESB_ECOLI | P23911 escherichia |
| 41 | 29 | 65.9 | 310 | 1 | ADPR_LACIA | Q06715 lactococcus |
| 42 | 29 | 65.9 | 326 | 1 | SCRR_PEDPE | P43472 pediococcus |
| 43 | 29 | 65.9 | 390 | 1 | SOX_MOUSE | Q9d826 mus musculu |
| 44 | 29 | 65.9 | 391 | 1 | ACKA_BACHD | Q9d815 bacillus ha |
| 45 | 29 | 65.9 | 395 | 1 | ACKA_BACSU | P37877 bacillus su |

RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*";
 RL Science 287:2183-2195(2000).
 CC -!- FUNCTION: PUTATIVE RECEPTOR THAT IS REQUIRED IN PHOTORECEPTOR
 CC CELLS PRECURSORS DURING EYE DEVELOPMENT.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name-Type 1;
 CC IsoId-P16376-1; Sequence=Displayed;
 CC Name-Type 2;
 CC IsoId-P16376-1; Sequence=External;
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN A SUBSET OF NEURAL PRECURSORS.
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR2
 CC subfamily.
 CC -----
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 CC -----
 CC EMBL; M28863; AAA62770.1; -;
 CC EMBL; AE003695; AAF54773.1; -;
 CC PIR; A32693; A32693.
 CC HSP; P19793; 2NLL.
 CC TRANSFAC; T02741; -;
 CC FlyBase; FBgn0003651; svp.
 CC GO; GO:0005737; P:cytoplasm; IDA.
 CC GO; GO:0007510; P:cardioblast cell fate determination; IEP.
 CC InterPro; IPR000536; Hormone_rec_lig.
 CC InterPro; IPR001723; Stdhmn_receptor.
 CC InterPro; IPR001628; Znf_C4steroid.
 CC Pfam; PF00104; hormone_rec; 1.
 CC Pfam; PF00105; zf-C4; 1.
 CC PRINTS; PR00398; STRDHORMONER.
 CC PRINTS; PR00047; STROIDFINGER.
 CC ProDom; PD000035; Znf_C4steroid; 1.
 CC SMART; SM00430; HOL1; 1.
 CC SMART; SM00399; Znf_C4; 1.
 CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 CC Zinc-finger; Vision; Alternative splicing.
 CC DNA_BIND 200 265 NUCLEAR RECEPTOR-TYPE.
 CC ZN_FING 200 220 C4-TYPE.
 CC ZN_FING 236 260 C4-TYPE.
 CC FT ZN_FING 236 260 C4-TYPE.
 CC SQ SEQUENCE 543 AA; 57987 MW; 0BC189DCF1A27213 CRC64;
 CC -----
 CC Query Match 77.3%; Score 34; DB 1; Length 543;
 CC Best Local Similarity 85.7%; Pred. No. 26;
 CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC -----
 CC QY 1 HOYLSSY 7
 CC | | | | |
 CC Db 305 HSYLSSY 311
 CC -----
 CC RESULT 2
 CC 7UP2_DROME STANDARD; PRT; 746 AA.
 CC ID P16376;
 CC DT 01-AUG-1990 (Rel. 15, Created)
 CC DT 01-NOV-1990 (Rel. 16, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Steroid receptor seven-up type 2.
 CC GN svp OR NR2F3.
 CC OS *Drosophila melanogaster* (Fruit fly).

CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; *Drosophila*.
 CC NCBI_TaxID=7227;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=90124631; PubMed=2105166;
 CC Mlodzik M., Hiroimi Y., Weber U., Goodman C.S., Rubin G.M.;
 CC "The *Drosophila* seven-up gene, a member of the steroid receptor gene
 CC superfamily, controls photoreceptor cell fates.";
 CC Cell 60:211-224(1990).
 CC -!- FUNCTION: PUTATIVE RECEPTOR THAT IS REQUIRED IN PHOTORECEPTOR
 CC CELLS PRECURSORS DURING EYE DEVELOPMENT.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name-Type 2;
 CC IsoId-P16376-1; Sequence=Displayed;
 CC Name-Type 1;
 CC IsoId-P16375-1; Sequence=External;
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN A SUBSET OF NEURAL PRECURSORS.
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR2
 CC subfamily.
 CC -----
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 CC -----
 CC EMBL; M28864; AAA03014.1; -;
 CC PIR; B32693; B32693.
 CC HSP; P19793; 2NLL.
 CC FlyBase; FBgn0003651; svp.
 CC InterPro; IPR000536; Hormone_rec_lig.
 CC InterPro; IPR001723; Stdhmn_receptor.
 CC InterPro; IPR001628; Znf_C4steroid.
 CC Pfam; PF00104; hormone_rec; 1.
 CC Pfam; PF00105; zf-C4; 1.
 CC PRINTS; PR00398; STRDHORMONER.
 CC PRINTS; PR00047; STROIDFINGER.
 CC ProDom; PD000035; Znf_C4steroid; 1.
 CC SMART; SM00430; HOL1; 1.
 CC SMART; SM00399; Znf_C4; 1.
 CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 CC Zinc-finger; Vision; Alternative splicing.
 CC DNA_BIND 200 265 NUCLEAR RECEPTOR-TYPE.
 CC ZN_FING 200 220 C4-TYPE.
 CC ZN_FING 236 260 C4-TYPE.
 CC SQ SEQUENCE 746 AA; 76830 MW; 7F256AFD4165326D CRC64;
 CC -----
 CC Query Match 77.3%; Score 34; DB 1; Length 746;
 CC Best Local Similarity 85.7%; Pred. No. 37;
 CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC -----
 CC QY 1 HOYLSSY 7
 CC | | | | |
 CC Db 305 HSYLSSY 311
 CC -----
 CC RESULT 3
 CC RPOD_ODOSI STANDARD; PRT; 1481 AA.
 CC ID P49468;
 CC DT 01-FEB-1996 (Rel. 33, Created)
 CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
 CC GN RPOC2.
 CC OS *Odontella sinensis* (Marine centric diatom).

OG Chloroplast.
 OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
 OC Biddulphiophycidae; Eupodiscales; Eupodisaceae; Odontella.
 OX NCBI_TaxID=2839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RT Kowalik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freier U.;
 RT "The chloroplast genome of a chlorophyll a+c-containing alga,
 RT Odontella sinensis.";
 RL Plant Mol. Biol. Rep. 13:336-342(1995).
 CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC (RNA)(N).
 CC -1- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four
 CC subunits: alpha, beta, beta', and beta".
 CC
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 CC
 CC EMBL: Z67753; CAA91746.1;
 CC PIR: S78373; S78373.
 CC HSP: O9KWU6; 1HQM.
 CC InterPro: IPR000722; RNA_pol_A.
 CC InterPro: IPR007066; RNA_pol_Rpbl_3.
 CC InterPro: IPR007083; RNA_pol_Rpbl_4.
 CC InterPro: IPR007081; RNA_pol_Rpbl_5.
 CC Pfam: PF04983; RNA_pol_Rpbl_3; 1.
 CC Pfam: PF05000; RNA_pol_Rpbl_4; 1.
 CC Pfam: PF04998; RNA_pol_Rpbl_5; 2.
 CC Transfaser; Transcription; DNA-directed RNA polymerase; Chloroplast.
 KW TRANSFERASE; Transcription; DNA-directed RNA polymerase; Chloroplast.
 SQ SEQUENCE 1481 AA; 170974 MW; 184936FB2A577228 CRC64;

Query Match 77.3%; Score 34; DB 1; Length 1481;
 Best Local Similarity 62.5%; Pred. No. 75;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSSYT 8

Db 924 HQFIDSYT 931

RESULT 4

ID CHIT_MANSE STANDARD; PRT; 554 AA.
 AC P36362;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Endochitinase precursor (EC 3.2.1.14).
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
 OC Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93357793; PubMed=8353525;
 RA Kramer K.J., Corpuz L., Choi H.K., Muthukrishnan S.;
 RT "Sequence of a cDNA and expression of the gene encoding epidermal and
 RT gut chitinases of Manduca sexta.";
 RL Insect Biochem. Mol. Biol. 23:691-701(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97215580; PubMed=9061927;
 RA Choi H.K., Choi K.H., Kramer K.J., Muthukrishnan S.;
 RT "Isolation and characterization of a genomic clone for the gene of an

RT Insect molting enzyme, chitinase.";
 RL Insect Biochem. Mol. Biol. 27:37-47(1997).
 CC -1- FUNCTION: DIGEST CHITIN IN THE EXOSKELETON DURING THE MOLTING
 CC PROCESS.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
 CC acetyl-D-glucosamine polymers of chitin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: EPIDERMIS AND GUT.
 CC -1- DEVELOPMENTAL STAGE: HIGH LEVELS SEEN IN THE EPIDERMIS ON DAY 0,
 CC BUT RAPIDLY DISAPPEARS AND IS UNDETECTED ON DAYS 1-4 OF FIFTH
 CC INSTAR. IT REAPPEARS ON DAY 5 AND PEAKS ON DAY 7 AFTER WHICH A
 CC RAPID DECLINE IS SEEN. IN THE GUT IS DETECTED ON DAY 6 WITH LOWER
 CC LEVELS SEEN ON DAYS 0, 7 AND 8.
 CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
 CC HYDROLASES).
 CC
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 CC
 CC EMBL: U02270; AAC04924.1;
 CC PIR: A56596; A56596.
 CC InterPro: IPR002557; Chitin_bind_PeRA.
 CC InterPro: IPR001223; Glyco_hydro_18.
 CC InterPro: IPR001579; Glyco_hydro_18/2.
 CC Pfam: PF01607; CBM_14; 1.
 CC Pfam: PF00704; Glyco_hydro_18; 1.
 CC ProDom: PD000471; Glyco_hydro_18; 1.
 CC SMART: SM00494; ChEBD2; 1.
 CC SMART: SM00636; Glyco_18; 1.
 CC PROSITE: PS01095; CHITINASE_18; 1.
 KW Hydrolase; Glycosidase; Chitin degradation; Signal; Glycoprotein.
 FT SIGNAL 1 19
 FT CHAIN 20 554
 FT DOMAIN 396 453
 FT ACT_SITE 146 146
 FT CARBOHYD 85 85
 FT CARBOHYD 303 303
 FT CARBOHYD 407 407
 FT CARBOHYD 545 545
 FT SEQUENCE 554 AA; 62203 MW; 3989D756C96CD490 CRC64;
 Query Match 75.0%; Score 33; DB 1; Length 554;
 Best Local Similarity 62.5%; Pred. No. 42;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLSSYT 8

Db 392 HKHMSST 399

RESULT 5

ID CLF_ARATH STANDARD; PRT; 902 AA.
 AC P93831; O80455;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Polycarb group protein CURLY LEAF.
 GN CLF OR AT2G23380 OR F26B6.3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.; FUNCTION, AND TISSUE SPECIFICITY.
 RC STRAIN=cv. Landsberg erecta; TISSUE=Flower;

RX MEDLINE-97205275; PubMed=9052779;
RA Goodrich J., Puangsomlee P., Martin M., Long D., Meyerowitz E.M.,
RA Coupland G.;
RT "A Polycomb-group gene regulates homeotic gene expression in
RA Arabidopsis";
RL Nature 386:44-51(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.X., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Morfat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RA thaliana";
RT Nature 402:761-768(1999).
CC -!- FUNCTION: Polycomb group (PCG) protein. Required to regulate
CC floral development by repressing the AGAMOUS homeotic gene in
CC leaves, inflorescence stems and flowers. PCG proteins act by
CC forming multiprotein complexes, which are required to maintain the
CC transcriptionally repressive state of homeotic genes throughout
CC development. PCG proteins are not required to initiate repression,
CC but to maintain it during later stages of development. They
CC probably act via the methylation of histones, rendering chromatin
CC heritably changed in its expressibility. May constitute the
CC catalytic subunit of a potential methyltransferase activity of PCG
CC complexes.
CC -!- SUBUNIT: Probable component of a PCG complex. In plants, PCG
CC complexes are probably composed of a member of the EZ family (CLF
CC or MEA), FIE, and a member of the VEFs family (FIS2, VRN2 or
CC EMF2) (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- TISSUE SPECIFICITY: Strongly expressed throughout the apical
CC meristem, leaf primordia, and leaves of 7-8 day-old seedling.
CC Weakly expressed in the vasculature of hypocotyl. Strongly
CC expressed throughout the young stages 1 and 2 floral meristems
CC that arose on the flanks of the apex. In stage 3 and 4 flowers, it
CC is expressed in the emerging sepal primordia and in the dome of
CC the floral meristem. During stages 6 and 7, it is strongly
CC expressed in developing petal and stamen, and weakly expressed in
CC the sepals. Late in floral development, at stage 12, it is weakly
CC expressed in all floral whorls, and expressed at intermediate
CC level in petals and ovules.
CC -!- DEVELOPMENTAL STAGE: Expressed in all four whorls throughout
CC flower development.
CC -!- SIMILARITY: BELONGS TO THE EZ FAMILY.
CC -!- SIMILARITY: Contains 1 SANT domain.
CC -!- SIMILARITY: Contains 1 SET domain.
CC -----
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CC -----
CC EMBL; Y10580; CAA71599.1; -;
CC EMBL; AC003040; AAC23781.1; -;
CC InterPro; IPR001005; MYB_DNA_binding.
CC DR InterPro; IPR001214; SET.
CC DR Pfam; PF00856; SET; 1.
CC DR SMART; SM00717; SANT; 1.
CC DR SMART; SM00317; SET; 1.
CC DR PROSITE; PS50280; SET; 1.
CC Transcription regulation; Repressor; Flowering; Nuclear protein;
CC Developmental protein.
CC DOMAIN 531 581 SANT.

FT DOMAIN 649 720 CYS-RICH.
FT DOMAIN 751 871 SET.
FT CONFLICT 225 225 S -> N (IN REF. 2).
FT CONFLICT 332 332 T -> P (IN REF. 2).
FT CONFLICT 415 415 K -> N (IN REF. 2).
FT CONFLICT 658 658 K -> Q (IN REF. 2).
FT CONFLICT 674 674 C -> Y (IN REF. 2).
FT CONFLICT 761 761 V -> I (IN REF. 2).
SQ SEQUENCE 902 AA; 100369 MW; 90B45ED27D219D64 CRC64;
Query Match 75.0%; Score 33; DB 1; Length 902;
Best Local Similarity 62.5%; Pred. No. 71;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 HOYLSSY 8
D 775 HEYLGEY 782
Db
RESULT 6
ID HEX8_ADEM1 STANDARD; PRT; 215 AA.
AC P19722;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Hexon-associated protein precursor (Protein VIII).
GN PVIII.
OS Mouse adenovirus type 1 (MAV-1).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90064816; PubMed=2531236;
RA Raviprakash K.S., Grunhaus A., el Kholy M.A., Horwitz M.S.;
RT "The mouse adenovirus type 1 contains an unusual E3 region.";
RL J. Virol. 63:5455-5458(1989).
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CC -----
CC EMBL; M30594; AAA42432.1; -;
CC PIR; A33382; SXADMS.
CC DR InterPro; IPR000646; Adeno_PVIII.
CC DR Pfam; PF01310; Adeno_PVIII; 1.
CC DR Hexon-associated protein.
CC FT PROPEP 1 109 POTENTIAL.
CC FT CHAIN 110 215 HEXON-ASSOCIATED PROTEIN.
CC FT SITE 109 110 CLEAVAGE (BY ADENOVIRUS PROTEASE)
CC (POTENTIAL).
CC SQ SEQUENCE 215 AA; 23272 MW; 739F0BE85408D7A1 CRC64;
Query Match 72.7%; Score 32; DB 1; Length 215;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYLSSY 7
D 198 HQFLSNY 204
Db
RESULT 7
ID KAD_CHLTR STANDARD; PRT; 245 AA.
AC O84130;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

```

DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN ADK OR CT128.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=D/UN-3/Cx;
RA MEDLINE=99000809; PubMed=97841136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
CC -1- FUNCTION: THIS SMALL UBQUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -1- SUBUNIT: Monomer (by similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the adenylate kinase family.
CC -----
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CC -----
CC EMBL; AE001286; AAC67719.1; -.
CC PIR; D71554; D71554.
CC HSSP; P08760; 2AK3.
CC HAMAP; MF_00235; -.
CC InterPro; IPR006259; Adenyl_kin_sub.
CC InterPro; IPR000850; Adenylate_kin.
CC Pfam; PF00406; ADK; 1.
CC PRINTS; PR00094; Adenylate_kinase.
CC ProDom; PD000657; Adenylate_kin; 1.
CC TIGRfams; TIGR01351; adk; 1.
CC PROSITE; PS00113; ADENYLATE_KINASE; 1.
CC Transferase; Kinase; ATP-binding; Complete proteome.
CC NE_BIND 12 20 ATP (BY SIMILARITY).
CC FT SEQUENCE 245 AA; 27784 MW; 3F38D306ED75D09F CRC64;
CC -----
CC Query Match 72.7%; Score 32; DB 1; Length 245;
CC Best Local Similarity 71.4%; Pred. No. 28;
CC Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC 1 HOYLSSY 7
CC 115 HEFLSSY 121
CC -----
DB SEPI1_SCHPO STANDARD; PRT; 663 AA.
AC Q43058; P79006;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Forkhead protein sepi1.
GN SEPI1 OR SPBC4C3.12.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98087410; PubMed=9427538;
RA Ribar B., Banrevi A., Sipiczki M.;
RT "sepi1+ encodes a transcription-factor homologue of the HNF-3/forkhead

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RT DNA-binding-domain family in Schizosaccharomyces pombe."
RL Gene 202:1-5(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=972;
RA MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitz E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Walther J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shipatowski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Contains 1 fork-head domain.
CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 86
CC TO 123, FROM POSITION 583 ONWARD AND IS SHORTER (586 AA) DUE TO
CC FRAMESHIFTS.
CC -----
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CC -----
CC EMBL; U88191; AAC49903.1; ALT_FRAME.
CC PIR; AL021730; CAA16826.1; -.
CC HSSP; T40493; T40493.
CC GeneDB_SPombe; SPBC4C3.12; -.
CC InterPro; IPR001766; TF_Fork_head.
CC Pfam; PF00250; Fork_head; 1.
CC PRINTS; PR00053; FORKHEAD.
CC ProDom; PD000425; TF_Fork_head; 1.
CC SMART; SM00339; FH; 1.
CC PROSITE; PS00657; FORK_HEAD_1; FALSE_NEG.
CC PROSITE; PS00658; FORK_HEAD_2; 1.
CC PROSITE; PS00039; FORK_HEAD_3; 1.
CC DNA-binding; Nuclear protein; Transcription regulation.
CC DNA_BIND 128 222 FORK-HEAD.
CC FT CONFLICT 377 387 VPSHLEKDVET -> TCITFEGGCCN (IN REF. 1).
CC SQ SEQUENCE 663 AA; 73031 MW; A66099437B7714C2 CRC64;
CC -----
CC Query Match 72.7%; Score 32; DB 1; Length 663;
CC Best Local Similarity 71.4%; Pred. No. 81;
CC Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CC -----
CC 1 HOYLSSY 7
CC 262 HOYLQNY 268
CC -----
DB SEPI1_SCHPO STANDARD; PRT; 663 AA.
AC Q43058; P79006;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Forkhead protein sepi1.
GN SEPI1 OR SPBC4C3.12.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98087410; PubMed=9427538;
RA Ribar B., Banrevi A., Sipiczki M.;
RT "sepi1+ encodes a transcription-factor homologue of the HNF-3/forkhead

```

```
RESULT 9
YATE_SCHPO STANDARD; PRT; 1628 AA.
AC Q09779; O13884;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein CID4.14 in chromosome I.
GN SPACID4.14 OR SPAC22F3.14C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Jayandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Welter J., Vansteelt E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RA "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: TO YEAST RLRL.
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-----
EMBL; Z69239; CAA93223.1; -
DR EMBL; Z54285; CAA91079.2; -
DR PIR; T38055; T38055.
DR GeneDB.SPombe; SPACID4.14; -.
KW Hypothetical protein.
SQ SEQUENCE 1628 AA; 188831 MW; 85A30FB43D2CAED0 CRC64;
Query Match 72.7%; Score 32; DB 1; Length 1628;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOYLSY 7
|:|:|:|
DB 1209 HRYLTSY 1215
RESULT 10
Y248_MYCGE STANDARD; PRT; 218 AA.
ID Y248_MYCGE
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CC -----
 CC EMBL; U28738; AAA68312.1; -
 DR PIR; T16951; T16951
 DR WormPep; T2809.3; CE02068.
 DR InterPro; IPR000326; PA_FTPase.
 DR Pfam; PF01569; PAP2; 1.
 DR SMART; SM00014; acldppc; 1.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 30 50 POTENTIAL.
 FT TRANSMEM 71 91 POTENTIAL.
 FT TRANSMEM 122 142 POTENTIAL.
 FT TRANSMEM 223 243 POTENTIAL.
 FT TRANSMEM 257 277 POTENTIAL.
 SQ SEQUENCE 341 AA; 39028 MW; DF74E39BC3E2DA8E CRC64;

Query Match 70.5%; Score 31; DB 1; Length 341;

Best Local Similarity 50.0%; Pred. NO. 63;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 HOVLSSYT 8

171 HRYITDYT 178

RESULT 12

ID SPSY_HUMAN STANDARD; PRT; 366 AA.
 AC P52788; O00544;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Spermine synthase (EC 2.5.1.22) (Spermidine aminopropyltransferase)
 DE (SPMSY).
 GN SNS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96027753; PubMed=7546290;
 RA Korhonen V.-P., Halmekytoe M., Kauppinen L., Myoehaenen S.,
 RA Wahlfors J., Keinonen T., Hyvoenen T., Alhonen L., Eloranta T.,
 RA Jaenne J.;
 RT "Molecular cloning of a cDNA encoding human spermine synthase.";
 RT DNA Cell Biol. 14:841-847(1995).
 [2]
 SEQUENCE FROM N.A.
 TISSUE=Colon;
 RX MEDLINE=97446142; PubMed=9299240;
 RA Grieff M., Whyte M.P., Thakker R.V., Mazzarella R.;
 RA "Sequence analysis of 139 kb in xp22.1 containing spermine synthase
 RT and the 5' region of PEX.";
 RL Genomics 44:227-231(1997).
 [3]
 SEQUENCE FROM N.A.
 TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP PARTIAL SEQUENCE.
 RA Eloranta T., Kajander O., Kauppinen L., Hyvoenen T.,
 RA Linnala-Kankkunen A., Kalkkinen N., Kulomaa M., Alhonen L.,
 RA Jaenne J.;
 RL (in) Goldemberg S.H., Algranati I.D. (eds.);
 RL Proceedings of the international symposium on the biology and
 RL chemistry of polyamines, pp.91-98, ICSU Press, New York (1988).
 CC -1- CATALYTIC ACTIVITY: S-adenosylmethioninamine + spermidine -> 5'-
 CC methylthioadenosine + spermine.
 CC -1- PATHWAY: BIOSYNTHESIS OF SPERMINE FROM SPERMIDINE.
 CC -1- SIMILARITY: BELONGS TO THE SPERMIDINE/SPERMINE SYNTHASES FAMILY.
 CC -----
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CC -----
 DR EMBL; Z49099; CAA88921.1; -
 DR EMBL; AD001528; AAB61308.1; -
 DR EMBL; BC009898; AAB09898.1; -
 DR PIR; S54160; S54160.
 DR Genew; HGNC:111123; SMS.
 DR MIM; 300105; -
 DR GO; GO:0004766; F:spermidine synthase activity; TAS.
 DR GO; GO:0006555; P:methionine metabolism; TAS.
 DR GO; GO:0006595; P:polyamine metabolism; TAS.
 DR InterPro; IPR001045; Sprmine synthase.
 DR Pfam; PF01564; Spermine synth; 1.
 DR PROSITE; PS01330; SPERMIDINE_SYNTHASE; 1.
 KW Transferase.
 FT DOMAIN 192 232 BINDING TO DECARBOXYLATED SAM
 FT (POTENTIAL).
 FT CONFLICT 1 1 M -> MPG (IN REF. 1).
 SQ SEQUENCE 366 AA; 41268 MW; D5B23EF61DE66443 CRC64;

Query Match 70.5%; Score 31; DB 1; Length 366;
 Best Local Similarity 62.5%; Pred. NO. 68;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOVLSSYT 8

45 HGYLATYT 52

RESULT 13

ID SPSY_MOUSE STANDARD; PRT; 366 AA.
 AC P97355;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Spermine synthase (EC 2.5.1.22) (Spermidine aminopropyltransferase)
 DE (SPMSY).
 GN SMS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strom T.M., Francis F., Lorenz B., Boeddrich A., Econs M.J.,
 RA Lehrach H., Meitinger T.;

RT *Pex gene deletions in Gy and Hyp mice provide mouse models for
RT x-linked hypophosphatemia*;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [2]

SEQUENCE FROM N.A.

RC TISSUE=Diaphragm;
RA Niranjan K., Korhonen V., Janne J.;
RT "Nucleotide sequence of mouse spermidine aminopropyltransferase
CDNA";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [3]

SEQUENCE OF 316-366 FROM N.A.

RX MEDLINE=98133937; PubMed=9467015;
RA Lorenz B., Francis F., Gempel K., Boeddrich A., Josten M., Schmah W.,
RA Schmidt J., Lehrach H., Meifinger T., Strom T.M.;
RT "Spermine deficiency in Gy mice caused by deletion of the spermine
synthase gene";
RL Hum. Mol. Genet. 7:541-547(1998).

CC -!- CATALYTIC ACTIVITY: S-adenosylmethioninamine + spermidine = 5'-
methylthioadenosine + spermine.

-!- PATHWAY: BIOSYNTHESIS OF SPERMINE FROM SPERMIDINE.

-!- SIMILARITY: BELONGS TO THE SPERMIDINE/SPERMINE SYNTHASES FAMILY.

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CC EMBL: Y09419; CAA70573.1;
DR EMBL: AF031486; AAB86631.1;
DR EMBL: AJ000093; CAA03919.1;
DR EMBL: AJ000087; CAA03918.1;
DR EMBL: AJ000088; CAA03918.1; JOINED.
DR EMBL: AJ000089; CAA03918.1; JOINED.
DR EMBL: AJ000090; CAA03918.1; JOINED.
DR EMBL: AJ000091; CAA03918.1; JOINED.
DR EMBL: AJ000092; CAA03918.1; JOINED.
DR MGD; MGI:109490; Sns.

GO: GO:0008215; P:spermine metabolism; IMP.

InterPro: IPR001045; Sperm_synthase.

Pfam: PF01564; Sperm_synth_1.

PROSITE: PS01330; SPERMIDINE_SYNTHASE; 1.

Transferrase.

FT DOMAIN 192 232 BINDING TO DECARBOXYLATED SAM

FT (POTENTIAL).

SEQUENCE 366 AA; 41313 MW; D549F319F31C43C5 CRC64;

Query Match 70.5%; Score 31; DB 1; Length 366;

Best Local Similarity 62.5%; Pred. No. 68;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSYST 8

| | | | |

45 HCVLATYT 52

RESULT 14

CGAL_CARAU

ID CGAL_CARAU STANDARD; PRT; 391 AA.

AC Q92161;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Cyclin A1 (Cyclin A).

GN CCN1 OR CCN4.

OS Carassius auratus (Goldfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Carassius.

OX NCBI_TaxID=7957;

RN [1]

SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RX MEDLINE=95377548; PubMed=7649388;

RA Katsu Y., Yamashita M., Hirai T., Tokumoto T., Kajiuura H.,

RA Nagahama Y.;

RT "Molecular cloning and immunological analysis of goldfish cyclin A

RL during oocyte maturation";

RL Dev. Biol. 170:616-625(1995).

CC -!- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF THE CELL CYCLE AT THE

CC G1/S (START) AND G2/M (MITOSIS) TRANSITIONS (BY SIMILARITY).

CC -!- SUBUNIT: INTERACTS WITH THE CDK2 AND THE CDC2 PROTEIN KINASES TO

CC FORM A SERINE/THREONINE KINASE Holoenzyme complex. THE CYCLIN

CC SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX (BY

CC SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.

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CC EMBL: S79215; AAB35103.1;

DR HSSP; P20248; LJSU.

DR InterPro: IPR006670; Cyclin.

DR InterPro: IPR004367; Cyclin_Cterm.

DR InterPro: IPR006671; Cyclin_N.

DR Pfam: PF00134; cyclin; 1.

DR Pfam: PF02984; cyclin; 1.

DR SMART: SM00385; CYCLIN; 2.

DR PROSITE: PS00292; CYCLIN; 1.

DR Cyclin; Cell cycle; Cell division; Mitosis.

KW SEQUENCE 391 AA; 43594 MW; 00402E02AFCB45F3 CRC64;

SQ

Query Match 70.5%; Score 31; DB 1; Length 391;

Best Local Similarity 62.5%; Pred. No. 73;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYLSYST 8

| | | | |

271 HQFLMQYT 278

RESULT 15

ATPA_CHLVU

ID ATPA_CHLVU STANDARD; PRT; 506 AA.

AC P56294;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE ATP synthase alpha chain (EC 3.6.3.14).

GN ATPA.

OS Chlorella vulgaris.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;

OC Chlorellaceae; Chlorella.

OX NCBI_TaxID=3077;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=TAM C-27 / Tamiya;

RX MEDLINE=97303241; PubMed=9159184;

RA Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,

RA Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T.,

RA Inamura A., Yoshinaga K., Sugiyama M.;

RT "Complete nucleotide sequence of the chloroplast genome from the

RT green alga Chlorella vulgaris: the existence of genes possibly

RT involved in chloroplast division";

RL Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).

CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON

CC GRADIENT ACROSS THE MEMBRANE. THE ALPHA CHAIN IS A REGULATORY

```

CC SUBUNIT.
CC -|- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
CC H(+)(Out).
CC -|- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -|- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
CC -|- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB001684; BAA57856.1; -.
CC PIR; T07209; T07209.
CC InterPro; IPR000793; ATPase_a/bc.
CC InterPro; IPR000194; ATPase_a/bcentre.
CC InterPro; IPR004100; ATPase_a/bn.
CC InterPro; IPR000790; ATPase_ac.
CC InterPro; IPR005294; ATPsynthF1_alpha.
CC Pfam; PF00006; ATP-synt_ab; 1.
CC Pfam; PF00306; ATP-synt_ab_C; 1.
CC Pfam; PF02874; ATP-synt_ab_N; 1.
CC ProDom; PD001099; ATPase_ac; 1.
CC TIGRFAMs; TIGR00962; atcpa; 1.
CC PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
CC ATP synthesis; Chloroplast; Thylakoid; Membrane; CF(1);
CC ATP-binding; Hydrolase; Hydrogen ion transport.
CC NP_BIND 170 177 ATP (POTENTIAL).
CC ACT_SITE 363 363 BY SIMILARITY.
CC SEQUENCE 506 AA; 54708 MW; 47A292DB3907F4FB CRC64;
CC -----
Query Match 70.5%; Score 31; DB 1; Length 506;
Best-Local Similarity 85.7%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYLSST 8
Db : 236 QYLSPT 242

```

Search completed: August 13, 2003, 09:45:45
 Job time : 26 secs

GenCore version 5.1.6
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OM protein, - protein search, using sw model

Run on: August 13, 2003, 09:43:01 ; Search time 96 seconds
(without alignments)
21.504 Million cell updates/sec

Title: US-10-056-052A-29
Perfect score: 44
Sequence: 1 HQVLSYST 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

al number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------|---------------------|
| 1 | 36 | 81.8 | 478 | 08F3B8 | 08f3b8 leptospira |
| 2 | 35 | 79.5 | 181 | 099PN5 | Q99pn5 mus musculus |
| 3 | 35 | 79.5 | 308 | 09CSC9 | Q9csc9 mus musculus |
| 4 | 35 | 79.5 | 356 | 08CEE2 | Q8cee2 mus musculus |
| 5 | 35 | 79.5 | 535 | 0922Y3 | Q922y3 mus musculus |
| 6 | 35 | 79.5 | 587 | 08R200 | Q8r2g0 mus musculus |
| 7 | 34 | 77.3 | 88 | 09PC98 | Q9pc98 xylella fas |
| 8 | 34 | 77.3 | 281 | 08T8U4 | Q8t8u4 drosophila |
| 9 | 34 | 77.3 | 468 | 09JVK7 | Q9jvk7 neisseria m |
| 10 | 34 | 77.3 | 493 | 09BMU6 | Q9bmuf aedes aegyp |
| 11 | 34 | 77.3 | 543 | 08MQJ1 | Q8mqj1 drosophila |
| 12 | 34 | 77.3 | 746 | 08INJ0 | Q8in10 drosophila |
| 13 | 34 | 77.3 | 1226 | 09S836 | Q58836 methanococ |
| 14 | 34 | 77.3 | 2531 | 016004 | Q16004 lytechinus |
| 15 | 33 | 75.0 | 113 | 008428 | Q08428 saccharomyc |
| 16 | 33 | 75.0 | 303 | 08DU06 | Q8du06 streptococ |

ALIGNMENTS

RESULT 1

08F3B8 ID Q8F3B8 PRELIMINARY; PRT; 478 AA.
AC Q8F3B8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT Arginate O-acetylation protein.
GN LA2489.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE011416; AAM49688.1;
KW Complete proteome.
SQ SEQUENCE 478 AA; 55633 MW; 745230B5BAD95BD1 CRC64;

Query Match 81.8%; Score 36; DB 16; Length 478;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQVLSYST 8

Db 177 HQFLESYT 184

RESULT 2

Q99PN5 ID Q99PN5 PRELIMINARY; PRT; 181 AA.
AC Q99PN5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tripartite motif protein TRIM29 (Fragment).
GN TRIM29.

Q9vn68 drosophila
Q969a9 bombyx mori
Q9pkm4 chlamydia m
Q9w6f5 gallus gall
Q9u916 chrysops sp
Q8mtk0 choristoneu
Q9ptj4 brachydanio
Q9fp07 oryza sativ
Q20826 caenorhabdi
Q8y2w1 anabaena sp
Q80455 arabidopsis
P93831 arabidopsis
Q9vn69 drosophila
Q8s4p6 zea mays (m
Q8h2g7 oryza sativ
Q9uux7 neurospora
Q8tsc6 methanosarc
Q8pvg7 methanosarc
Q9vpw4 drosophila
Q8tnt8 methanosarc
Q8tts9 methanosarc
Q8tts7 methanosarc
Q9qb00 anticarsia
Q9ddq5 decapterus
Q9ddq9 decapterus
Q9ddq0 decapterus
Q9ddq1 decapterus
Q9ddq3 decapterus

```
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21231161; PubMed=11331580;
RA Raymond A., Meroni G., Fantozzi A., Merla G., Cairo S., Luzi L.,
RA Riganelli D., Zanaria E., Messali S., Cainarca S., Guffanti A.,
RA Minucci S., Pellicci P.G., Ballabio A.;
RT "The tripartite motif family identifies cell compartments.";
RL ENBO J. 20:2140-2151(2001).
RL EMBL; AF230390; AAG50169.1; -.
DR MGD; MGI:1919419; Trim29.
FT NON_TER 1
FT NON_TER 181
FT SEQUENCE 181 AA; 20724 MW; 37B9F326AFAAC71 CRC64;

Query Match 79.5%; Score 35; DB 11; Length 181;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSYST 8
Db 110 HRYMNSYST 117

RESULT 3
Q9CSC9 PRELIMINARY; PRT; 308 AA.
ID Q9CSC9;
AC Q9CSC9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 2810431N19RIK protein (Fragment).
GN TRIM29 OR 2810431N19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Embryo;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Harai A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Mikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK013219; BAB28721.1; -.
DR MGD; MGI:1919419; Trim29.
FT NON_TER 1
FT SEQUENCE 308 AA; 35316 MW; E7F6EB6C8414228C CRC64;

Query Match 79.5%; Score 35; DB 11; Length 308;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

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QY 1 HOYLSYST 8
Db 169 HRYMNSYST 176

RESULT 4
Q8CEE2 PRELIMINARY; PRT; 356 AA.
ID Q8CEE2;
AC Q8CEE2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Tripartite motif protein 29.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Skin;
RC MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK028448; BAC25956.1; -.
DR EMBL; AK028448; BAC25956.1; -.
DR SEQUENCE 356 AA; 40966 MW; 3A8E01AB7D1FAE28 CRC64;

Query Match 79.5%; Score 35; DB 11; Length 356;
Best Local Similarity 62.5%; Pred. No. 47;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSYST 8
Db 217 HRYMNSYST 224

RESULT 5
Q922Y3 PRELIMINARY; PRT; 535 AA.
ID Q922Y3;
AC Q922Y3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Unknown (Protein for IMAGE:3498575) (Fragment).
GN TRIM29.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC006699; AAH06699.1; -.
DR MGD; MGI:1919419; Trim29.
DR InterPro; IPR000315; Znf_Bbox.
DR Pfam; PF00643; zf-B_box; 1.
DR SMART; SM00336; BBOX; 2.
DR PROSITE; PS00119; zF-BBOX; 1.
FT NON_TER 1
FT SEQUENCE 535 AA; 60575 MW; 4D7081FCD39B7BAE CRC64;

Query Match 79.5%; Score 35; DB 11; Length 535;
Best Local Similarity 62.5%; Pred. No. 72;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSYST 8
Db 396 HRYMNSYST 403
```

RESULT 6

Q8R200 PRELIMINARY; PRT: 587 AA.
 AC Q8R200;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to tripartite motif-containing 29.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC027353; AAH27353.1; -.
 DR InterPro: IPR000315; Znf_Bbox.
 DR Pfam: PF00643; Zf-B_box; 1.
 DR SMART: SM00336; BBOX; 2.
 PROSITE: PS01119; ZF_BBOX; 1.
 SEQUENCE 587 AA; 65819 MW; D6E5C65F6A05EA98 CRC64;

Query Match 79.5%; Score 35; DB 11; Length 587;

Best Local Similarity 62.5%; Pred. No. 80;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSYST 8

Db 448 HRYMNSYT 455

RESULT 7

Q9PC98 PRELIMINARY; PRT: 88 AA.
 AC Q9PC98;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein Xf1883.
 GN Xf1883
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylella.
 OX NCBI_TaxID=2371;
 [1]
 RN SEQUENCE FROM N.A.
 RA STRAIN=9a5c;
 MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvares J.G., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Honeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kurnae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Martins A.M.B.N., Madeira H.M.F., Marinho C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.2., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshahko M.H.,

RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
 RL Nature 406:151-159(2000).
 DR EMBL: AE004008; AAF84689.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 88 AA; 9913 MW; 3EEAB9A47B358CAA CRC64;

Query Match 77.3%; Score 34; DB 16; Length 88;

Best Local Similarity 75.0%; Pred. No. 17;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSYST 8

Db 15 HOYISSLT 22

RESULT 8

Q8T8U4 PRELIMINARY; PRT: 281 AA.
 AC Q8T8U4; O9VGA9;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE AT29920p (CG11502 protein).
 GN SVP OR CG11502 OR CG18158.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 [1]
 RN SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RA STRAIN=Berkley;
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yeandle M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burks K.C., Busam D.A., Butler H., Chao E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., McLeod M.P., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzay D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Sequence 287:2185-2195(2000).
[3]
SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattel B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragad V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirkas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of *Drosophila melanogaster* genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of *Drosophila melanogaster* genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY075272; AAL68139.1; -;
DR EMBL; AE003695; AAF54774.2; -;
DR HSP; P19793; ILBD
DR FlyBase; FBgn0003651; svp.
DR InterPro; IPR000536; Hormone_rec_lig.
DR Pfam; PF00104; hormone_rec; 1.
DR SMART; SM00430; HOL1; 1.
SQ SEQUENCE 281 AA; 31347 MW; F604481821AB7259 CRC64;

Query Match 77.3%; Score 34; DB 5; Length 281;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSSY 7
DB 43 HSYLSSY 49

RESULT 9
Q9JVK7 PRELIMINARY; PRT; 468 AA.
AC Q9JVK7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative two-component system sensor kinase (EC 2.7.3.-).
GN NMA0797.
OS Neisseria meningitidis (serogroup A).

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Davies S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* 22491.";
RL Nature 404:502-506(2000).
CC -1- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
DR EMBL; ALI62754; CAB84080.1; -;
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR003660; HAMP.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00512; Hiska; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR SMART; SM00304; HAMP; 1.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00388; Hiska; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
KW Kinase; Phosphorylation; Sensory transduction; Transferase;
KW Complete proteome.
SQ SEQUENCE 468 AA; 52804 MW; 47FD3A0BC67416B2 CRC64;

Query Match 77.3%; Score 34; DB 16; Length 468;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSSY 8
DB 93 HRYIDSY 100

RESULT 10
Q9BMU6 PRELIMINARY; PRT; 493 AA.
AC Q9BMU6
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Nuclear hormone receptor.
OS Aedes aegypti (yellow fever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Aedes.
OX NCBI_TaxID=7159;
RN [1]
SEQUENCE FROM N.A.
RA Zhu J., Miura K., Dittmer N.T., Raikhel A.S.;
RT "A mosquito homolog of chicken ovalbumin upstream promoter transcription factor represses the 20-hydroecdysone response during vitellogenesis.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
DR EMBL; AF303224; AAG53940.1; -;
DR HSP; P19793; 2NLL.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Steroid_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMNER.

DR PRINTS: PR00047; STROIDFINGER.
 DR PRODom: PD000035; Znf_C4steroid; 1.
 DR SMART: SM00430; HOLI; 1.
 DR SMART: SM00399; Znf_C4; 1.

DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
 * KW Transcription regulation; Zinc; Zinc-finger.
 SQ SEQUENCE 493 AA; 54072 MW; 02AED5107CD2B45C CRC64;

Query Match 77.3%; Score 34; DB 5; Length 493;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSSY 7

Db 255 HSYLSSY 261

RESULT 11

QBMQJ1 PRELIMINARY; PRT; 543 AA.

QBMQJ1

DT 01-OCT-2002 (T-EMBLrel. 22, Created)

DT 01-OCT-2002 (T-EMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)

DE R080410P.

SV OR CG11502 OR CG18158.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OC NCBI_TaxID=7227;

SEQUENCE FROM N.A.

STRAT-Berkeley;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,

RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,

RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,

RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Celniker S.

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.

EMBL: AY129452; AAM76194.1; -

DR FlyBase: FBgn003651; svp.

DR InterPro: IPR000536; Hormone_rec_lig.

DR InterPro: IPR001723; Stdrhm_receptor.

DR InterPro: IPR001628; Znf_C4steroid.

DR Pfam: PF00104; hormone_rec; 1.

DR Pfam: PF00105; zf-C4; 1.

DR PRINTS: PR00398; STRDHORMONER.

DR PRINTS: PR00047; STROIDFINGER.

DR PRODom: PD000035; Znf_C4steroid; 1.

DR SMART: SM00430; HOLI; 1.

DR SMART: SM00399; Znf_C4; 1.

KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;

* KW Transcription regulation; Zinc; Zinc-finger.

SQ SEQUENCE 543 AA; 58047 MW; DD04FD10042C2D3C CRC64;

Query Match 77.3%; Score 34; DB 5; Length 543;

Best Local Similarity 85.7%; Pred. No. 1.2e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HOYLSSY 7

Db 305 HSYLSSY 311

RESULT 12

Q8INJ0 PRELIMINARY; PRT; 746 AA.

ID Q8INJ0

AC Q8INJ0;

DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DE CG11502-PA.
 GN SVP.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 SEQUENCE FROM N.A.
 RP MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burlis K.C., Busam D.A., Butler H., Chretien E., Center A., Chandra I.,
 RA Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foslter C., Gabrieli A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Meout S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodagat, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 SEQUENCE FROM N.A.
 RP Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galie R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of Drosophila melanogaster genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 SEQUENCE FROM N.A.
 RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,

RA Ciamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RT "Annotation of *Drosophila melanogaster* genome.",
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RP Adams M.D., Celnikier S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE FROM N.A.
 RA FlyBase;
 RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003695; AN13541.1; D6085838A848087B CRC64;
 SQ SEQUENCE 746 AA; 76814 MW; 6085838A848087B CRC64;

 Query Match 77.3%; Score 34; DB 5; Length 746;
 Best Local Similarity 85.7%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 1 HQYLSSY 7
 | | | | |
 Db 305 HSYLSSY 311

 RESULT 13
 Q58836 PRELIMINARY; PRT; 1226 AA.
 AC Q58836;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein MJ1441.
 GN MJ1441.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.D., Geoghagen N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, *Methanococcus*
 RT *jannaschii*.",
 RL Science 273:1058-1073(1996).
 CC -1- SIMILARITY: STRONG TO P.DENITRIFICANS COBN AND M.JANNASCHII
 CC MJ0907.
 DR EMBL: U67585; AAB99452.1; -
 DR TIGR: MJ1441; -
 DR InterPro: IPR003672; COBN/Mg-*chl*tase.
 DR Pfam: PF02514; COBN-Mg-*chel*; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1226 AA; 141327 MW; 8F7DDF4E36162AB9 CRC64;

 Query Match 77.3%; Score 34; DB 17; Length 1226;
 Best Local Similarity 71.4%; Pred. No. 2.8e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 1 HQYLSSY 7
 | | | | |
 Db 509 HQYIASY 515

 RESULT 14
 Q58836 PRELIMINARY; PRT; 1226 AA.
 AC Q58836;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein MJ1441.
 GN MJ1441.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.D., Geoghagen N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, *Methanococcus*
 RT *jannaschii*.",
 RL Science 273:1058-1073(1996).
 CC -1- SIMILARITY: STRONG TO P.DENITRIFICANS COBN AND M.JANNASCHII
 CC MJ0907.
 DR EMBL: U67585; AAB99452.1; -
 DR TIGR: MJ1441; -
 DR InterPro: IPR003672; COBN/Mg-*chl*tase.
 DR Pfam: PF02514; COBN-Mg-*chel*; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1226 AA; 141327 MW; 8F7DDF4E36162AB9 CRC64;

 Query Match 77.3%; Score 34; DB 5; Length 2531;
 Best Local Similarity 62.5%; Pred. No. 6.2e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 1 HQYLSSY 8
 | | | | |
 Db 949 HEYVDSY 956

 RESULT 15
 Q08428 PRELIMINARY; PRT; 113 AA.
 AC Q08428; O00018;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE ORF YOR053W.
 GN YOR053W OR YOR29-04.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE OF 1-8 FROM N.A.
 RA Landt O., Hiesel R., Unseld M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

O16004 PRELIMINARY; PRT; 2531 AA.
 AC O16004;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Notch homolog.
 OS *Lytechinus variegatus* (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Topopneustidae;
 OC *Lytechinus*.
 OX NCBI_TaxID=7654;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97454256; PubMed=9310331;
 RA Sherwood D.R., McClay D.R.;
 RT "Identification and localization of a sea urchin Notch homolog:
 RT Insights into vegetal plate regionalization and Notch receptor
 RT regulation.",
 RL Development 124:3363-3374(1997).
 DR EMBL: AF000634; AAB82088.1; -
 DR HSSP: P01132; IEGF.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF-Ca.
 DR InterPro: IPR001438; EGF-II.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR000800; Notch.
 DR Pfam: PF00023; ank; 6.
 DR Pfam: PF00008; EGF; 35.
 DR Pfam: PF00066; notch; 3.
 DR PRINTS: PR01415; ANKYRIN.
 DR PRINTS: PR00010; EGF_BLOOD.
 DR PRINTS: PR01452; NOTCH.
 DR SMART: SM00248; ANK; 5.
 DR SMART: SM00179; EGF_CA; 23.
 DR SMART: SM00004; NL; 3.
 DR PROSITE: PS50088; ANK_REPEAT; 5.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 21.
 DR PROSITE: PS00022; EGF_1; 33.
 DR PROSITE: PS01186; EGF_2; 25.
 DR PROSITE: PS01187; EGF_CA; 20.
 KW ANK repeat; EGF-like domain; Repeat.
 SQ SEQUENCE 2531 AA; 273982 MW; 5BF42BEC627CA303 CRC64;

 Query Match 77.3%; Score 34; DB 5; Length 2531;
 Best Local Similarity 62.5%; Pred. No. 6.2e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 1 HQYLSSY 8
 | | | | |
 Db 949 HEYVDSY 956

 RESULT 15
 Q08428 PRELIMINARY; PRT; 113 AA.
 AC Q08428; O00018;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE ORF YOR053W.
 GN YOR053W OR YOR29-04.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE OF 1-8 FROM N.A.
 RA Landt O., Hiesel R., Unseld M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RA Bohn C., Bolotin-Fukuhara M., Daignan-Fornier B., Dang D.V.,
 RL Valens M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97279235; PubMed=9133743;
 RA Valens M., Bohn C., Daignan-Fornier B., Dang V., Bolotin-Fukuhara M.;
 RT "The sequence of a 54.7 Kb fragment of yeast chromosome XV reveals the
 RL presence of two tRNAs and 24 new open reading frames.";
 RL Yeast 13:379-390(1997).
 DR EMBL; 274961; CAA99245.1; -;
 DR EMBL; 270678; CAA94538.1; -;
 DR SCD; S0005579; YOR053W.
 DR SEQUENCE 113 AA; 15256 MW; D4841A26AA5FB64C CRC64;

Query Match 75.0%; Score 33; DB 3; Length 113;
 Best Local Similarity 85.7%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSY 7
 Db 82 HQYRSSY 88

Search completed: August 13, 2003, 09:47:29
 Job time : 99 secs

